STIC-Biotech/ChemLib

56040

From:

Swope, Sheridan

Sent:

Thursday, June 09, 2005 6:04 PM

To:

STIC-Biotech/ChemLib

Subject:

10023515

For 10023515, pls search and interference search:

SID 1 against the NT and AA data bases.

SID 2 against the NT and AA data bases. SID 3 against the NT and AA data bases.

Sheridan Swope, Ph.D. Patent Examiner, AU 1652 Recombinant Enzymes 571-272-0943 (voice) E02B71 Remsen Bld (Office) E02C70 Remsen Bld (Mailbox)

STAFF USE ONLY

Searcher:_ Searcher Phone: 2-Date Searcher Picked up:_ Date Completed:_ Searcher Prep/Rev. Time:_ Online Time:_

Type of Search

NA#:	AA#:
Interference:	SPDI:
S/L:(Oligomer:
Encode/Trans	sl:
Structure#:_	Text:
inventor:	Litigation:

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Maximum Match 100%
Listing first 45 summaries
UniProt_03:*
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ALIGNMENTS

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MEDLINE-2238857; PubMed-12477932; DOI=10.1073/pnas.242603899;

Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casvant F.L., Scheetz T.E.,

A Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramoon R.D., Mullahy S.J.,

A Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Hitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,

A Kones S. T. Marra M.A.
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05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
FLJ31547 protein.
Name=FLJ31547;
Hydrolase.
SEQUENCE
                                                                                                           TISSUE=PCR rescued clones;
Director MGC Project;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the type-B carboxylesterase/l
EMBL; BC069501; AAH69501.1; -.
HSSP; P12337; 1K4Y.
GO; GO:0003824; F:catalytic activity; IEA.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs.
                                        Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
                                                                                                                                                                                                                                                                                                                                                                    Jones S.J., Marra M.A.; "Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 and mouse cDNA sequences."; proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Query Match Best Local

Similarity

94.7%;

Length

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X PubMed=14702039; DOI=10.1038/ng1285;

Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

Wa Makamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

Wa Wakamatsu A., Hayashi K., Sato H., Nagai X., Kimura K., Makita H.,

Wa Wakamatsu J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,

Wa Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,

Wa Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,

Wa Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,

Wa Yamamoto J., Saito K., Kawai Y., Isono H., Sugawara M.,

Wa Yamamoto J., Kaku Y., Kodaira H., Kono H., Sugawara M.,

Wa Yamashi K., Yamaa H., Kawa M., Yamazaki M.,

Wa Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,

Wa Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,

Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,

Ra Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
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Name=FL/31547;
Homo sapiens (Human).
Bukaryota; Metazoa; C.
Mammalia; Eutheria; P
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01-DEC-2001 (TrEMBLrel. 19, Createq)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation updat
Hypothetical protein FLJ31547.
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diacchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diacchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Moriya S., Sench A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe K., Kumagai A., Takemoto M., Kawakami B.,
RA Fujimori Y., Komiyama M., Tashiro H., Taniyami A., Pujiwara T.,
RA Fujimori Y., Komiyama M., Tashiro H., Taniyami A., Pujiwara T.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Nakai K., Yada T., Namura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Namura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
T. Tomplete sequencing and characterization of 21,243 full-length human
                                                                                                                                                              Query Match
Best Local Similarity
Matches 501; Conser
                                                                                                                                                                                                                                        GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR0032018; CarbesteraseB.
InterPro; IPR003279; Ser_estrs.
InterPro; IPR00379; Ser_estrs.
Pfam; PF00135; COesterase; 1.
PROSITE; BS00122; CARBOXYLESTERASE_B_1; 1.
PROSITE; BS00941; CARBOXYLESTERASE_B_2; 1.
Hydrolase; Hypothetical protesin.
SEQUENCE 525 AA; 58200 MW; 7724878B8A22F215 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2004) to the EMBL/GenBe-
-- SIMILARITY: Belongs to the type-B
EMBL; AK056109; BAB71094.1; --
EMBL; BC069548; AAH69548.1; --
EMBL; P12337; 1K4Y.
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Strausberg R.;
Submitted (APR-2004) to th
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nilarity 90.9%;
Conservative (
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the type-B carboxylesterase/lipase
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REATSYPNICLONSEWLLLDOHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWF

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RX PubMedal4702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayshi K., Sato H., Nagai K., Kimura K., Makita H.,
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RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa K., Yamazaki M.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa K., Fujimori K.,
RA Alo K., Takiguchi S., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Tanai H., Kimata M., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Saro S.,
RA Moriya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Yamazaki M., Watanabe T., Sugiyama A., Takami S., Terashima Y., Suzuki O.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Matsumura K., Nawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
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Q8NBC8; Createc
01-OCT-2002 (TrEMBLrel. 22, Last sc
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01-OCT-2003 (TrEMBLrel. 25, Last ar
Hypothetical protein FLJ33678.
Homo sapiens (Human).
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TISSUE=Brain;
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RESULT 4
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DE Cart
GN Name
OC Euka
OC Mamma
OX NCBJ
RN [1]
RN [1]
RN [1]
RN S[1]
RN Miya

Name=cauxin

Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9615;

Canis familiaris (Dog). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Carnivora;

Craniata; Vei ; Fissipedia;

Vertebrata; ia; Canidae;

Euteleostomi;

SEQUENCE FROM N.A.
Miyazaki M., Yamashita T.,
"cauxin family protein.";

Taira

Ή;

Q6AW47 PRELIMINARY; PRT; 575 AA. Q6AW47; 25-OCT-2004 (TrEMBLrel. 28, Created) 25-OCT-2004 (TrEMBLrel. 28, Last sequence up 25-OCT-2004 (TrEMBLrel. 28, Last annotation Carboxylesterase-like urinary excreted prote

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-- SIMILARITY: Belongs to the

EMBL; AK090997; BAC03565.1; -.

HSSP; P12337; 1K4Y.
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PROSITE; PS00122; CARBOXYLESTERASE_B_1;
PROSITE; PS00941; CARBOXYLESTERASE_B_2;
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InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs.
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                                                                                                                  LKGDIVMFEGATEEEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMS
                                                                                                                                                                                                                               LGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2454; DB 2;
Pred. No. 7.8e-179;
2; Mismatches 0;
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                                                    D Q6AW46 PRELIMINARY; PRT; >/> ra.

C Q6AW46;
T 25-OCT-2004 (TrEMBLrel. 28, Created)
T 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
T 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
T 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
C Carboxylesterase-like urinary excreted protein.
N Name=cauxin;
N Name=cauxin;
Nus musculus (Mouse).
S Mus musculus (Mouse).
C Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ex
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; N
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Best Local Similarity
Matches 417; Conser
                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: Belongs to the type-B carboxylesterase/lipase EMBL; ABI86392; BaD35015.1; --- GO; GO:0003824; F:catalytic activity; IEA.
InterPro; IPR0002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs.
Ffam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
Hydrolase.
SEQUENCE 575 AA; 63620 MW; 1005C35E82E1183D CRC64;
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       FROM N.A.
M., Yamashita
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TRPAFVKADHSDEIRFVFGGAFLKGNIVMFEGATEEEKLLSRKMMRYWANFARTGDPNGE
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Pred. No. 4e-163;
1; Mismatches 7
                                                                       Craniata; Vertebrata; Sciurognathi; Muridae;
     Η.,
       Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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; Murinae; Mus
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 RESULT 6
Q8103
ID Q810
AC Q810
DT 01-M
DT 01-M
DT 01-M
CR Carbo
GN Name
GN NAM
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Q8I034;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Carboxylesterase-like urinary excreted protein.
                                               Felis silvestris catus (Cat).
Eukaryota, Metazoa, Chordata, Craniata, Ven
Mammalia, Eutheria, Carnivora, Fissipedia,
 SEQUENCE
                    NCBI_TaxID=9685;
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FROM

N.A.

Vertebrata; ia; Felidae;

Euteleostomi; Felis.

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Query Match
Best Local s
Matches 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "cauxin family protein.";

Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
EMBL; AB186393; BAD35016.1; -.
GO; GO:0003824; F:catalytic activity; IEA.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR00379; Ser_estrs.
PROSITE; PS00112; CARBOXYLESTERASE_B 1; 1.
PROSITE; PS00112; CARBOXYLESTERASE_B 2; 1.
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SEQUENCE
    546
                      552
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90; Conservative
                                      RKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIPL
                                                                             ILSASDMLHSPLSSLTFLSLLQPFFFFCA
                                                                                                                                                            KTKSFTRVVDGAFFDNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMKEAPEILSGSNKS
                                                                                                                                                                                                     HRAIMQSGVAIIPSLKSSDNDLKHDLQVVANVCDCNVSDSKALLKCLREKSSLELMSLSQ
                                                                                                                                                                                                                 WCFFLILQPILGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAP
                                                                                                                                                                                                                                                                                                                                                                         WIFGAILE-----
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                                                                                                                                                                                                                                                                                                                                                                                                             Score 2094.5; DI
Pred. No. 3e-151;
59; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                       3EB9D85981D9DE0A CRC64;
                    580
 574
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RESULT
Q95KH3
ID Q99
AC Q9
AC Q9
DT 011
DT 011
DT 01
DT 01
OC CC
OX MA
OC CC
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"Molecular cloning and characterization of a novel carboxylesterase-
"Ike protein that is physiologically present at high concentrations in

It the urine of domestic cats (Felis catus).";

Biochem. J. 370:101-110(2003).

"L. Biochem. J. 370:101-110(2003).

"EMBL; AB045377; BAC22577.1; -.

"EMBL; AB045377; BAC22577.1; -.

"EMBL; AB045377; Fhydrolase activity; IEA.

"R INSP; P12337; IXY.

"GO; GO:0016787; Frhydrolase activity; IEA.

"InterPro; IPR002018; CarbesteraseB.

"InterPro; IPR002079; Ser estrs.

"InterPro; IPR002079; Ser estrs.

"PAGNITE; PS00122; CARBOXYLESTERASE B 1; 1.

"PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OEC-2001 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu Mammalia; Eutheria; Primates; Catarrhini; Cercopitheci Cercopithecinae; Macaca.
NCBI_TaxID=9541;
                                                                                                                                                                                                                                           Q95KH3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Kidney;
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Local Similarity 71.7%;
nes 373; Conservative 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGGAFKMGSASSFDGSALAAYEDVLIVTTQYRLGIFGFFDTGDEHARGNWALLDQVAALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REATSYPNLCLQNSEWLLLDQHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFE 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VALLTOKAFNSVPSIIGVNNHECAFLL-STEFSBILGGSNRSLALYLVHTFLNIPTQYLH
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Pred. No. 6.5e-
60; Mismatches
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                                                    Cercopithecidae;
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                                                                                  Euteleostomi;
                                                                                                         monkey)
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RESULT 8

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Best Local
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-!- SIMILARITY: Belongs to the type-B carboxylesterase/1
EMBL; AB060973; BAB46884.1; -.
HSSP; P12377; 1K4Y.
InterPro: Tenangar
                                                                                                                                                                                                                                                                                                            SASB ANAPL
Q04791;
01-FEB-1995
Anas platyrhynchos (Domestic duck).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Archosauria; Aves; Neognathae; Anseriformes; Anatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002018; CarbesteraseB.
Pfam; PF00135; COesterase; 1.
Hypothetical protein.
SEQUENCE 361 AA; 41032 MW: AC62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=Temporal lobe right;
Osada N., Hida M., Kusuda J.,
                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE TISSUE=Uropygial gland; MEDLINE=9300823; PubMed=8314791;
                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
25-CCT-2004 (Rel. 45, Last amotation update)
Fatty acyl-CoA hydrolase precursor, medium ch
                                                                                                                                                                                                           NCBI_TaxID=8839;
                                                                                                                                                                                                                                                               (Thioesterase B).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTK 301
                                                                                                                                                                                                                                                                                                                                                                                               VEFWTSTIPLILSASDTLHSPLSFLIPLSLLQPFFFSCVP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFE
                                                                                                                                                                                                                                                                                                                                                                                                                   VDFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFFCAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEILSGSNKSLALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDGLLDLLGDVFFVVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSKELLTLSQKAKSFTRVVDGAFFPNEPLGLLSQKAFKAIPSIIGVNNHECGFLLPM-EA
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                                                                                                                                                                                                                                                                                                                                        STANDARD;
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95.0%;
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                                                                                                                                                                                                                                      Euteleostomi;
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Query Match
Best Local Similarity
Matches 265; Conser
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PIR; A47162; A47162.

HSSP; O77540; 1K4Y.

InterPro; IPR002018; CarbesteraseB.

InterPro; IPR00279; Ser_estrs.

Pfam; PP00135; COesterase; 1.

PROSITE; PS00122; CARBOXYLESTERASE_B_2; 1.

PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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 550
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RRRKHTDL 557
                                                                                                                                     VYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEKLLSRKMM
                                                                                                                                                                                                  LHI-----PPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAP
                                                                                                                                                                                                                                                  GAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLP-MKEAPEILSGSNKSLALHLIQNI
                                                                                                                                                                                                                                                                                                                                                   LREATSYPNICLONSEWILLDOHML-----KVHYPKFGVSEDCLYLNIYAPAHADTGSKL
                             SDMLHSPL
                                                                              KYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIPLILSA 555
                                                                                                                  VYFYEFQHRPSSAAGVVPEF
                                                                                                                                                                                                                                 GVFFPKSPRQLLSEKVINAVPYIIGVNNCEFGWILPRMMKFPEFTEGLEKDVÅRQVLQST
                                                                                                                                                                                                                                                                                                 LFTE---
                                                                                                                                                                                                                                                                                                                       PYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKEL--LTLSQKTKSFTRVVD
                                                     KYWTNFARNGNPNGEGLVHWPQYDMDERYLEIDLTQKAAKKLKERKMEFWMQLTEQIMSD
                                                                                                                                                                         LALSFKGAPSDIVDLVYNEYIGVAENRAQVRDGLLDSIADPLFVFSAVEVARHHRDAGNP
                                                                                                                                                                                                                                                                                                                                                                                                             PVFVWIHGGGLVSGAASSYDGSALAAFDNVVVVTIQYRLGIAGYFSTGDKHARGNWGYLD
                                                                                                                                                                                                                                                                                                                                                                                                                             PVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VRDAASYPPMCLQDK----VLGQYLSDAITNRKEKVRLQISEDCLYLNVYTPVSTEEQEKL
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llarity 48.4%;
Conservative 79
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Acyl-ester intermediate (By Sil
Charge relay system (By Sil
Charge relay system (By Sil
By Similarity.
N-linked (GlcNAc. . .) (Pol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1298.5; DB 1;
Pred. No. 1.9e-90;
9; Mismatches 177;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; DB 1;
.9e-90;
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  (By similarity).
  (By similarity).
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RESULT

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RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Liver;

RX MEDLINE=22744052; PubMed=12859986; DOI=10.1016/S0003-9861(03)00286-8;

RX MEDLINE=22744052; PubMed=12859986; DOI=10.1016/S0003-9861(03)00286-8;

RX MEDLINE=22744052; PubMed=12859986; DOI=10.1016/S0003-9861(03)00286-8;

RX MEDLINE=22744052; PubMed=12859986; DOI=10.1016/S0003-9861(03)00286-8;

RT Purification, molecular cloning, and functional expression of rinducible mouse liver acylcarnitine hydrolase in C57BL/6 mouse, belonging to the carboxylesterase multigene family.";

RT belonging to the the carboxylesterase/lipase family. C1-1. SIMILARITY: Belongs to the type-B carboxylesterase/lipase family. DR EMBL; BC01529; AAH345290.1; -...

DR EMBL; BC034170; AAH34178.1; -...

DR EMBL; BC034180; AAH34178.1; -...

DR EMBL; BC034191; AAH34180.1; -...

DR EMBL; BC034191; AAH34191.1; -...

DR EMBL; AB110073; BAC76623.1; -...
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RC STRAIN=FYB/N; TISSUB=COlon, and Kidney;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Hopkins R.F., Jordan H., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Hopkins R.F., Jordan R., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Hopkins R.F., Jordan R., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Hopkins R.F., Jordan R., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Hopkins R.F., Jordan R., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Brownstein M.J., McEwan R.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Brownstein M.J., McEwan R.J., Madan A., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Holting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Geners J., Marra M.A.,"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=FVB/N; TISSUE=Colon, and Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=FVB/N; TISSUE=Colon; Strausberg R.; Submiffor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q91WG0 PRELIMINARY; PRT; 561 AA.
Q91WG0;
Q91WG0;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Carboxylesterase 2 (Carboxylesterase ML3 precursor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Kidney;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Generation and initial analysis of more than 15,000 and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Best Local
                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
NISS musculus 11 days pregnant adult female ovary and uterus cDNA,
NISS musculus 11 days pregnant adult female ovary and uterus cDNA,
NISS MUSCULUSTERASE (E 3.1.1.1) (ALI-ESTERASE) (B-ESTERASE)
(MONOBUTYRASE) (COCAINE ESTERASE) (PROCAINE ESTERASE) (METHYLBUTYRASE)
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GO:0005615; C:extrace; 1.
PEROSITE; PS00122; CARBOXYLESTERASE B 1; 1.
PROSITE; PS09941; CARBOXYLESTERASE B 2; 1.
                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                    (9030624L02Rik protein)
Name=9030624L02Rik;
                                                                                                                                                                                                                                                                                                                                      Q8BK48;
                                                                                                                                                                                                                                                                                                                                                                 Q8BK48
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                                                                             Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VVPALITARYHRDAGAPVYFYBFRHRPQCFBDTKPAFVKADHADBVRFVFGGAF--LKGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N---KSLALHLIQNILH-----IPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKAGRLQFWTKTLPQKIQELKASQDKHREL
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27
561 AA;
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                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -TBEEBLLSRRMMKYWANFARHGNPNSEGLPYWPVMDHDEQYLQLDIQPAVGRA
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62469
                             Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X.
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                       Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                             Euteleostomi;
; Murinae; Mus
                                                                                                                                                          (METHYLBUTYRASE)
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C STRAIN-C57BL/6J; TISSUE-Ovary and uterus;

A Adachi J., Aizawa K., Akhmura T., Arakawa T., Bono H., Carninci P.,

A Hayashida K., Hayatsu N., Hiramoto K., Hiracka T., Hirozane T.,

A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nokamura M.,

A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka

A Tagawa A., Takahashi F., Takaka-Akahira S., Takeda Y., Tanaka T.,

A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899; Strausberg R. L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-C57BL/6J; TISSUE-Ovary and uterus;

MEDLINS-20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishiro T., Harada A.,

Yamamoto R., Matsumoto H., Sakyunzzama M., Nishine T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
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STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs
prepare full-length cDNA libraries for rapid discovery of new
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                               STRAIN=FVB/N; TISSUE=Colon;
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The FANTOM Consortium,
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"High-efficiency full-length c
Meth. Enzymol. 303:19-44(1999)
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STRAUENCE FROM N.A.
STRAUN-C57BL/60; TISSUE-OVARY and N
MEDLINE-99279253; PubMed-10349636;
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MEDLINE=21085660;
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420:563-573(2002).
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; DOI=10.1038/35055500
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; DOI=10.1016/S0076-6879(99)03004-9;
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on functional annotation
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Best Local :
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MGD; MGI:244310; 9030624L02Rik.

GO; GO:0005615; C:extracellular space;
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-2003) to the EMB-I- SIMILARITY: Belongs to the EMBL; AK077248; BAC36707.1; -- EMBL; BC055062; AAH55062.1; --
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STRAIN=FVB/N; TISSUE=Colon;
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              YWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIP
                                                              YFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMK
                                              M-----LPPECGDLLMEEYMGDTEDPETLQAQFREMKGDFMFVIPALQVAHFQR-SHAPV
                                                                                                                      IQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPV
                                                                                                                                               GELMASKDFHPVPSIIGINNDEYGWILPTIMDPAQKIEEITRKTLPAVL----KSTALKM
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                                                                                                                                                                                                                                                                                                                  FPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAAL
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Pred. No. 4.2e-89;
9; Mismatches 165;
99:16899-16903 (2002)
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A., Schein J.
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G.G.,
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C STRAIN-Syrian golden; TISSUE=Liver;
C STRAIN-Syrian golden; Takabatake E., Wang C., Isobe M.;
A Sone T., Ishida Y., Takabatake E., Wang C., Isobe M.;
A Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
C -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase fam.
EMBL; D50577; BAA23605.1; -.

R HSSP; P12337; IK4Y.
R GO; GO:0016787; F:carboxylesterase activity; IEA.
R GO; GO:0016787; F:hydrolase activity; IEA.
R GO; GO:0016787; F:hydrolase activity; IEA.
R GO; GO:0016787; F:hydrolase activity; IEA.
R InterPro; IPR0002018; CarbesteraseB.
R InterPro; IPR0000886; ER_target S.
R InterPro; IPR0000886; ER_target S.
R InterPro; IPR0000886; ER_target S.
R InterPro; IPR000089; Ser_target S.
R InterPro; IPR000089; Ser_target S.
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Best Local Similarity
Matches 262; Conserv
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O35533;
O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Carboxylesterase precursor (EC 3.1.1.1).
Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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SIGNAL
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PROSITE; PS00941; CARBOXYLESTERASE B 2;
PROSITE; PS00941; ETARGET; UNKNOWN 1.
Hydrolase circuit
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STRAIN-Syrian golden; TISSUE=Liver;
Sone T., Wang C.Y.;
"Microsomal amidases and carboxylesterases.";
(In) Guengerich F.F. (eds.);
COMPREHENSIVE TOXICOLOGY VOLUME 3, Biotransfo;
Pergamon, Oxford (1997).
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HRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWATFA
                                                                                                                                                NEPLDLLSQKAFKAIPSIIGVNNHECGFLLP--MKEAPEILSGSNKSL--ALHLIQNILH
                                                                                              I PPQYLHLVANEYFHDKHSLTBIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFR
                                                  LPPECGDLLMEEYMGDNEDPQTLQAQFREMMGDFTFVIPSLQVAHFQR-AHAPVYFYEFQ
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Q1-MAR-2003 (TrEMBLrel. 23, Created)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 25, Last sequence update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male colon cDNA, RIKEN full-length enriched
Library, clone:9030624L02 product:similar to CARBOXYLESTERASE (EC
3.1.1.1) (ALI-ESTERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAINE ESTERASE)
(PROCAINE ESTERASE) (METHYLBUTYRASE).
                                                                                                                        MEDLINE-2053091; PubMed-i1076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watatahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Muramateu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771 (2000).
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STRAIN=C57BL/60; TISSUE=Colon;

MEDLINB=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

Carninc1 P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10:1617-1630(2000).
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TISSUE=Colon;
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
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STRAIN=C57BL/6J; TISSUE=Colon;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annot 60,770 full-length cDNAs."; Nature 420:563-573(2002).
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Nature 409:685-690(2001)
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STRAIN=C57BL/6J; TISSUE=Colon;
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RESULT Q6PDB7 ID Q6 AC Q6 D7 01 D7 05 D7 05 D7 05 D7 05

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Q6PDB7; Q6PDB7; 05-JUL-2004 (05-JUL-2004 (05-JUL-2004 (Hypothetical

(TrEMBLrel. 27, Created)
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RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katch H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Myazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Salto R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,
RA Tomaru A., Tokahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
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YWATFARTGNPNGNDLSLWPAYNLTEQYLOLDLNMSLGQRLKEPRVDFWTSTIP
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48.7%; Pred. No. 2.4e-88;
tive 78; Mismatches 166; Indels
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Morrey K.C., Hale S., Garcia A.M., Gay L.J., Hulpk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulpk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 273; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPRO02018; CarbesteraseB.
InterPro; IPRO0379; Ser estrs.
Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.
PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Hypothetical protein.
SEQUENCE 556 AA; 61927 MW; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SIMILARITY: Belongs to the type-B carboxylesterase/lipase EMBL; BC058815; AAH58815.1; - HSSP; P12337; IK4Y.
GO: GO: 0016787; F:hydrolase activity; IEA.
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                SHVVSPMSKGLFHGAIMESGVALLPYLITDTSEMVS-
                                                                                                                                                                                          SSLILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVNVFLGVPFAAPPLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHMLKVHY 118
RGKSEAEILAINKLVOMIPAVVDGEFFFRHFKELLASEDFHPVFSIIGVNNDEFGWTIF-
                                                                                                                                                                                                                                                              IQYRLGVLGFFSTGDQHARGNWGFLDQVAALRWIQQNIAHFGGKPDRVTIFGESAGGTSV
                                                                                                                                                                                                                                                                                                                PPVSTSEDCLYLNIYTPAHAHEGSNLPVMVWIHGGGLVAGMASMYDGSLLAAIEDLVVVT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVHTFLGI PFAKPPVGPLRFAPPEAPEFWSGVRDGTAHPAMCLQN----LGVMKEIKLKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MPQGLTSSASQWCFFLI--LQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPV
                                                                                                                                                                                                                                                                                                                                                                                                                                          PKFGVSEDCLYLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.1%; Score 1266.5; DB 2;
47.1%; Pred. No. 5.3e-88;
cive 76; Mismatches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A. 99:16899-16903(2002)
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse I.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner I., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner I., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Robak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Rillon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Maters M., Touchman J.W., Grenn E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Klein S., Gerhard D.S.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the type-B carboxylesterase/l
EMBL; BC074230; AAH74330.1; -.
GO; GO:0016787; F:hydrolase activity; IEA.
                                                                                                                         SEQUENCE
                                                                                                                                                                                                                  Richardson
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                         Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                             initiative.
                                                                                                                                                                                   "Genetic and genomic tools initiative.":
                                                                                                                                                                                                                                                        MEDLINE=22341132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Name=LOC443703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q6GM54;
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                                                                                                                       FROM N.A.
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                                                                                                                                                         225:384-391 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                PubMed=12454917; DOI=10.1002/dvdy.10174;
Bberg R.L., Wagner L., Pontius J., Clifto
                                                                                                                                                                                                for
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Last annotation updat
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                                                                                                                                                                                            Xenopus
                                      carboxylesterase/lipase
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                                                                                                                                                                                                                                Clifton S.W.,
                                                                                                                                                                                          NIH Xenopus
                                      tamily.
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Best Local S
Matches 258
O70177 PRELIMINARY; PRT; 561 AA.
070177;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Carboxylesterase precursor (EC 3.1.1.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs.
Pfam; PP00135; COGSTECTASE; 1.
PROSITE; PS00122; CARBOXYLESTERASE B 1;
PROSITE; PS00941; CARBOXYLESTERASE_B_2;
                                                                                                                                                                                                                                         Rattus norvėgicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                             Name=carboxylesterase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KYWANFARNGDPNGLGLAEWPKYDEDEDYLEIKLTQESSQRLKGGRFKFWTVTLP
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Best Local Sim.
Matches 275;
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InterPro; IPR000379; Ser_estrs.
Pfam; PF00135; COesterase; 1.
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         completed: June
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                                                                                                                       ISVSSLILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQ-VVAHFCGNNASDSEAL
                                                                                                                                                                                                                                                                                                    VVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGA 235
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                                                           LDLNMSLGQRLKEPRVDFWTSTIP
                                                                                  VF-GSFFSGMKLDF---
                                                                                                                                                                 TIPMVMGTAQIIKE----LSRENLQAVLKDTAAQMMLPPECGDLLMEEYMGNTDDSQTLQ
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                                                                                                                                                                                                                                                 TSVSSHVISPMSQGLFHGAIMESGVALLPDLIS---ETSETVSTTVAKLSGCEAMDSBAL
                                                                                                                                                                                                                                                                                                                                                                                                                   MPRNQLHSWLNAVLFGLLL--LLIHVQ-GQDSPES-SPIRTTHTGQVQGKLDHVKDTKAG
                                         LDTHPAVDRALKARRLQFWTKTLP
                                                                                                                                                                                                                                                                                          VVTIQYRLGVLGFFSTGDEHARGNWGYLDQVAALRWVQQNIAHFGGNPNRVTIFGESAGG
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          2005,
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                                                                                  -TEEERLLSRRMMKYWANFARQGNPNSEGLPYWPALDHDEQYLQ
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         09:39:21
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Pred. No. 1.1e-87;
77; Mismatches 179
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Maximum Match 100%
Listing first 45 summaries
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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(without alignments)
2236.078 Million cell updates/sec
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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?	Qy 3	Qy 2 Qy 2 Qy 3		B & B &	Query Matc Best Local Matches 2	RESULT 1 A47162 thiolestera C;Species: C;Date: 05- C;Accession C;Accession A;Title: Mo A;Reference A;Accession A;Status: p A;Molecula A;Residues: A;Cross-ref C;Keywords: F;56-545/Do	•	30 643 31 633 627 334 594 43 5569 575 569 575 569 575 575 575 575 575 575 575 575 575 57
	381 LHIPPQYLHLVANEYFHI :	64 PYLEAHDYEKSEDLOWAHFOG 50 LFTEQPEEQAQRIAAAAG 22 GAFFPNEPLDLESQKAFKAIPS 23 [95	30 TGPSAEGPORNTRLGWIQGKQVTVLG	ch 42.2%; l Similarity 48.4%; 265; Conservative 7	RESULT 1 A47162 thiolesterase B (BC 3) precursor - C;Species: Anas platyrhynchos (mallard) C;Date: 05-May-1995 #sequence_revision 0 C;Accession: A47162 R;Hwang, C.S.; Kolattukudy, P.E. Biol. Chem. 269, 14278-14284, 1933 A;Title: Molecular cloning and sequencin A;Feference number: A47162; MUID:9330082 A;Accession: A47152 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-557 <hwa> A;Residues: 1-557 <hwa> A;Cooss references: UNIPROT:004791; GB:L C;Superfamily: cholinesterase; cholinest C;Keywords: hydrolase F;56-545/Domain: cholinesterase homology</hwa></hwa>	1	643.5 20.9 597 2 A33668 633.5 20.6 599 2 A57701 627.5 20.4 664 2 JC7990 618 20.1 612 2 A34967 594.5 19.3 691 2 JE0150 598 19.3 550 1 S47639 581.5 18.9 767 2 A25363 572.5 18.6 602 2 T37254 570.5 18.6 637 2 S66236 569.5 18.5 557 2 A566236 569.5 18.5 557 2 A566236 569.5 18.5 557 2 A566236 569.5 18.3 545 2 A89046 557.5 18.1 593 1 S25062 557.5 18.1 593 1 S25062
	LHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAP :	F E E	KG KG YE	TGPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAPPLGSLRFTNPQPASPWDN	Score 1298.5; DB 2; Length Pred. No. 4.1e-94; Polynomial Process of the Prediction o	recursor - mallard (mallard) (mallard) revision 05-May-1995 #text_change 3. 1993 sequencing of thioesterase B cDN (D:9300823; PMID:8314791 cholinesterase homology homology <che></che>	ALIGNMENTS	
TAMERICA CONTACT	ALITARYHRDAGAP 435 : : avevarhhrdagap 435	LILSOKTKSETRVVD 321	, H—H D—D	LRETNPOPASPWDN 89 : : : : : : : : : :	ch 557; s 27; Gaps 8;	nge 09-Jul-2004 CDNA and stimulation of expre		sterol esterase (E sterol esterase (E acetylcholinestera sterol esterase (E acetylcholinestera crystal protein pr acetylcholinestera acetylcholinestera acetylcholinestera acetylcholinestera acetylcholinestera acetylcholinestera acetylcholinestera brotein grote esterase - Caenorh protein B0238.1 [i triacylglycerol li esterase precursor

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436 VYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMM 495

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R,Ozols, J.
J. Biol. Chem. 264, 125
A,Title: Isolation, pro
A;Reference number: A34
A,Accession: A34329
A;Status: preliminary
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A; Cross-references: UNIPROT: P14943
A; Cross-references: UNIPROT: P14943
C; Superfamily: cholinesterase; cholinesterase homology
C; Keywords: carboxylic ester hydrolase
F; 32-517/Domain: cholinesterase homology <CHE>
F; 201, 430/Active site: Ser, His #status predicted
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Best Local Similarity
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       468
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HIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEF
                                                                                                                                                                                                                                                                                             NIAHFGGNPGRVTIFGESAGGTSVSSHVLSPMSQGLFHGAIMESLVALLPGLITSSSEVV
                                                                                                                                                                                                                                                                                                                                                     LTMGMASMYDGSALAAFEDVVVVTIQYRLGVLGFFSTGDQHATGNHGYLDQVAALRWVQK
                                                                                                                                                                                                                                                                                                                                                                       FKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALSWVQK 214
                                                         QHRPSFTKDLRPPHVRADHGDEVVFVFRSHLFGSKVPL----TEEEELLSRRVMKYWANF
                                                                                      RHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMKYWATF
                                                                                                                                                                                                       QKAFKAIPSIIGVNNHECGFLLP------MKEAPEILSGSNKSLALHLIQNIL
                                                                                                                                                                                                                                     S--TVVANLSRCGQVDSETLVRCLRAKSEEEMLAITQVFMLIPGVVDGVFLPRHPEELLA
                                                                                                                                                                                                                                                              EDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEPLDLLS
                                                                                                                                                                                                                                                                                                                         NIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKS
                                                                                                                     --PPALGDLLMDEYMGSNEDPKHLMAQFQEMMADAMFVMFALRVAHLQR-SHAPTYFYEF
                                                                                                                                                                            LADFQPVPSIIGINNDEYGWIIPKLLLAIDPQEERDRQAMREIMHQATKQLML------
                                                                                                                                                                                                                                                                                                                                                                                                               PAMCÜQN--LAIMDQDVLLLHFTPPSIPMSEDCLYLNIYSPAHAREGSDLPVMVWIHGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                  PNICLQNSEWILLDQHMLKVHY--PKFGVSEDCLYLNIYAPAHADTGSKLPVILVWFPGGA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIRNTHTGQVRGSLVHVEGTDAGVHTFLGIPFAKPPLGPLRFAPPEPAEAWSGVRDGTSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PORNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAPPLGSLRFTNPQPASPWDNLREATSY 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KYWTNFARNGNPNGEGLVHWPQYDMDERYLEIDLTQKAAKKLKERKMEFWMQLTEQIMSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12533-12545, 1989 properties, and the complete amino acid A34329; MUID:89308686; PMID:2745458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.0%; Score 1231.5; DB 2;
47.8%; Pred. No. 7.2e-89;
tive 76; Mismatches 167;
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A;Residues: 1-559 <SCH>
A;Cross-references: UNIPROT:O00748; GB:Y09616; NID:g2058317; PIDN:CAA70831.1; PID:g205831
A;Experimental source: intestine
C;Comment: This enzyme hydrolyzes many xenobiotics, such as carboxyl esters, thioesters & C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Schwer, H.; Langmann, T.; Daig, R.; Becker, A.; Aslanidis, C.; Schmitz, Biochem. Biophys. Res. Commun. 233, 117-120, 1997
A;Title: Molecular cloning and characterization of a novel putative carbo: A;Reference number: JC5408, MUID:97289502; PMID:9144407
A;Accession: JC5408
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C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JC5408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: GDB: CES2; iCE; CE2
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Best Local
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                                                                                                                                                                                                                                                             FFPNEPLDLISQKAFKAIPSIIGVNNHECGFLLP----MKEAPEILSGSNKSLALHLIQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NFARNGNPNGEGLPHWPLFDQEEQYLQLNLQPAVGRALKAHRLQFWKKALP
                       TFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIP
                                                                                 FOHQPSWLKNIRPHMKADHGDELPFVF-RSFFGGNYIKF
                                                                                                                 EFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKWMKYWA 499
                                                                                                                                                         LLMLPPTFGDLLREEYIGDNGDPQTLQAQFQEMMADSMFVIPALQVAHF-QCSRAPVYFY 436
                                                                                                                                                                                                  ILHIPPOYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFY 439
                                                                                                                                                                                                                                        FLPRHPQELLASADFQPVPSIVGVNNNEFGWLIPKVMRIYDTQKEMDREASQAALQKMLT 377
                                                                                                                                                                                                                                                                                                                       LIA----SSADVISTVVANLSACDQVDSEALVGCLRGKSKEEILAINKPFKMIPGVVDGV 317
                                                                                                                                                                                                                                                                                                                                                           LEAHDYEKSEDL--QVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGA 323
                                                                                                                                                                                                                                                                                                                                                                                                      VAALRWVQQNIAHFGGNPDRVTIFGESAGGTSVSSLVVSPISQGLFHGAIMESGVALLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                  VAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIPY 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDGTTHPAMCLQDLTAVESEFL----SQFNMTFPSDSMSEDCLYLSIYTPAHSHEGSNLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GQDSASPIRTTHTGQVLGSLVHVKGANAGVQTFLGIPFAKPPLGPLRFAPPEPPESWSGV 85
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46.7%; Pred. No. 1e-88;
vative 91; Mismatches 168;
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S47655

Carboxylesterase (EC 3.1.1.1) precursor - golden hamster C;Species: Mesocricetus auratus (golden hamster) C;Date: 26-Dec-1994 #sequence_revision 03-Aug-1995 #text_C;Accession: S47655

#text_change

09-Jul-2004

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A;Molecule type: mRNA
A;Residues: 1-561 <SON>
A;Cross - references: UNIPP
C;Superfamily: cholinestc
C;Keywords: carboxylic es
F;58-546/Domain: cholines
F;227,459/Active site: S6
Carboxylesterase (EC 3.1.1.1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S34607
R;Aida, K.; Moore, R.; Negishi, M.
Biochim. Biophys. Acta 1174, 72-74, 1993
A;Title: Cloning and nucleotide sequence of a novel, male-predominant carboxylesterase A;Reference number: S34607; MUID:93326638; PMID:7916639
A;Accession: S34607
A;Accession: S34607
A;Residues: preliminary
A;Molecule type: mRNA
A;Residues: 1-554 <AID-
A;Cross-references: UNIPROT:Q63880; GB:S64130; NID:g404388; PIDN:AAB27606.1; PID:g40438
C;Keywords: carboxylic ester hydrolase
C;Keywords: carboxylic ester hydrolase
F;46-536/Domain: cholinesterase homology <CHE>
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S34607
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Blochim. Blophys. Acta 1207, 138-142, 1994
A;Title: Cloning and sequence analysis of a hamster liver cDNA encoding a A;Reference number: S47655; MUID:94318665; PMID:8043605
A;Recession: S47655
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F;215,443/Active site: Ser, His #status predicted
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-554 <OVN>
A;Cross-references: UNIPROT:P23953; GB:M57960; NID:g192853; PIDN:AAA63297.1; PID:g192854
A;Cross-references: UNIPROT:P23953; GB:M57960; NID:g192853; PIDN:AAA63297.1; PID:g192854
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase
C;Keywords: cholinesterase homology <CHE>
F;50-540/Domain: cholinesterase homology <CHE>
                                                                                                                                                                                                                         C;Accession: A39060
R;Ovnic, M; Tepperman, K.; Medda, S.; Elli
Genomics 9, 344-354, 1991
A;Title: Characterization of a murine cDNA
A;Reference number: A39060; MUID:91169540;
                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
A39060
                                                                                                                                                                                                                                                                                                   carboxylesterase (BC 3.1.1.1) precursor -
C;Species: Mus musculus (house mouse)
C;Date: 06-Mar-1992 #sequence_revision 06-
C;Accession: A39060
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37.8%; Score 1163; DB 2;
44.3%; Pred. No. 1.9e-83;
tive 84; Mismatches 193;
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46.5%; Pred. No. 2.7e-85;
tive 81; Mismatches 183;
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16 LILQPLLGHRQWGKTGBSAEGPQRNTRLGWIQGKQVTVLGSPVBVNVFLGVBFAAPBLGS

75

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A;Molecule type: protein
A;Nolecule type: protein
A;Note: 28-Lys and 33-Leu were also found
C;Superfamily: cholinesterase; cholinesterase homology
C;Superfamily: cholinesterase; endoplasmic reticulum; glycoprotein; homotrimer
C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; homotrimer
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-566/Product: carboxylesterase #status experimental <MAT>
F;51-552/Domain: cholinesterase homology <CHE>
F;80/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;222,467/Active site: Ser, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                       carboxylesterase (EC 3.1.1.1) precursor - pig
N;Alternate names: proline-beta-naphthylamidase
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C;Accession: S19307; S23607
R;Matsushima, M.; Inoue, H.; Ichinose, M.; Tsukada, S.; Miki, K.; Kurokawa,
PBBS Lett. 293, 37-41, 1991
     &
                                S
                                                                                                                                                                                                                                                                                                                                            PEBS Lett. 293, 37-41, 1991
A;Title: The nucleotide and deduced amino acid sequences of porcine liver proline-beta-r
A;Reference number: S19307; MUID:92070571; PMID:1959668
A;Accession: S19307
                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q29550; A;Accession: S23607
                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-566 < MAT1>
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                                 WCFFLILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAP
 WLLPLVLTSLASSATW--AGQPASPPVVDTAQGRVLGKYVSLEGLAQPVAVFLGVPFAKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFW 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EHSPGNWAHLDQLAALRWVQDNIANFGGNPDSVTIFGESSGGISVSVLVLSPLGKDLFHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>LRFAPPOPAEPWSFVKNATSYPPMCSODAGWAKILSDMFSTEKEILPLKISEDCLYLNIY</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EETNLSKMVMKFWANFARNGNPNGEGLPHWPEYDEQEGYLQIGATTQQAQRLKAEEVAFW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -QKTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPM---KEAPE-IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AISESGVVINTNVGKKNIQAVNEIIATLSQC--NDTSSAAMVQCLRQKTESELLEISGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPADLTKSSQLPVMVWIHGGGLVIGGRSPYNGLALSAHENVVVVTIQYRLGIWGLFSTGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAVCPILGH-----SLLPPVVDTTQGKVLGKYISLEGFEQPVAVFLGVPFAKPPLGS
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                                                                                                                                                                                                                                                                                                                                                                                                                       H.; Ichinose, M.; Tsukada, S.; Miki, K.; Kurokawa, K.;
                                                                                      44.3%;
                                                                                                     37.8%;
                                                                   Score 1162.5; DB
Pred. No. 2.1e-83;
1; Mismatches 202
                                                                                                                                                                                                                                                                                                            EMBL: X63323; NID: g1930;
                                                                                                  2
                                                                   Indels
                                                                                                  Length
                                                                                                                                                                                                                                                                                                            PIDN: CAA44929.1;
                                                                  41;
                                                                  Gaps
   59
                                   71
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Carboxylesterase (EC 3.1.1.1) El precursor, minor form - rat
Carboxylesterase (EC 3.1.1.1) El precursor, minor form - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Av
C;Accession: JX0054
R;Takagi, Y.; Morohashi, K.; Kawabata, S.; Go, M.; Omura, T.
J. Biochem. 104, 801-806, 1988
A;Title: Molecular cloning and nucleotide sequence of cDNA of microsomalization of the complex 
                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 238
                                                                                                                                                                                                                                                                                                                                                                     :221,453/Active site: Ser, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   527
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                  76
                                                                                  11 LAVCPIWGH-----PSSP-PVVDTTKGKVLGKYVSLEGFTQPVAVFLGVPFAKPPLGS
                                                                                                                                                              16
                                                                                                                                                                                                                                     238;
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                                                                                                                                                                                                                                                                   Similarity
LRFTNPQPASPWDNLREATSYPNLCLQN-----SEWLLLDQHMLKVHYPKFGVSBDCL 128
                                                                                                                                                  LILOPLIGHROWGKTGPSAEGPORNTRIGWIQGKQVTVLGSPVPVNVFLGVPFAAPPLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QIGVNTQAAKRLKGEEVAFWNDLL 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QLDLNMSLGQRLKEPRVDFWTSTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVR 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KDLFLDLMGDVVFGVPSVTVARQHRDAGAPTYMYEFQYRPSFSSDKKPKTVIGDHGDEIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QEFGWLLPTMMGFPLSEGKLDQKTATSLLWKSYP1AN1PEELTPVATDKYLGGTDDPVKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HECGFLLPMKEAPEILSGS-NKSLALHLION---ILHIPPQYLHLVANEYFHDKHSLTEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELLTLSQKTKSFT------RVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNN
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                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                            37.2%; Score 1144; DB 2; 43.5%; Pred. No. 5.8e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----APBEEVSLSKTVMKFWANFARSGNPNGEGLPHWPMYDQEEGYL
                                                                                                                                                                                                                              92;
                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   549
                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                          34;
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                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           predicted
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YLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGF 188

LRFAPPEPAEPWSFVKNTTTYPPMCSQDGVVGKLLADMLSTGKESIPLEF----SEDCL

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A, Molecule type: mRNA
A; Residues: 61-567 < LON>
A; Cross-references: GB: M55509; NID:g179929; PIDN:AAA35650.1; PID:g179930
R; Shibata, F.; Takagi, Y.; Kitajima, M.; Kuroda, T.; Omura, T.
Genomics 17, 76-82, 193
A; Title: Molecular cloning and characterization of a human carboxylesterase gene.
A; Reference number: A47376; MUID:94010913; PMID:8406473
A; A; Residues: nucleic acid sequence not shown; not compared with conceptual translation
A; Molecule type: mRNA; DNA
A; Residues: 1-3, PALV', 8-11, 'A', 13-567 < SHI>
A; Cross-references: GB: D21088; NID:g455476; PIDN:BAA04650.1; PID:g458470
A; Note: sequence extracted from NCBI backbone (NCBIP:137630) and corrected to correspond
R; Zschunke, F.; Salmassi, A.; Kreipe, H.; Buck, F.; Parwaresch, M.R.; Radzun, H.J.
Blood 78, 506-512, 1991
A; Title: cDNA cloning and characterization of human monocyte/macrophage serine esterase-
A; Reference number: A49816; MUID:91300111; PMID:2070086
A; Molecule type: mRNA
A; Residues: 'G', 65-185, 'G', 187-361, 363-567 < ZSC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carboxylesterase (EC 3.1.1.1) precursor, monocyte/macrophage [validated] - human N;Alternate names; carboxylesterase, hepatic; monocyte/macrophage serine esterase C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C;Accession: A41010; JH0327; Ā47376; A49816; PS0280; I61085; A48809; I57004
R;Munger, J.S.; Shi, G.P.; Mark, E.A.; Chin, D.T.; Gerard, C.; Chapman, H.A.
J. Biol. Chem. 266, 1882-18838, 1991
A;Title: A serine esterase released by human alveolar macrophages is closely related A;Reference number: A41010; MUID:92011649; PMID:1918003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P23141; GB:M73499; NID:g179927; PIDN:AAA35649.1; PID:g179928 A;Note: parts of this sequence, including the amino end of the mature protein, were conf R;Long, R.M.; Calabrese, M.R.; Martin, B.M.; Pohl, L.R. Life Sci. 48, PL43-PL49, 1991 A;Title: Cloning and sequencing of a human liver carboxylesterase isoenzyme. A;Reference number: JH0327; MUID:91148424; PMID:1997784 A;Accession: JH0327; MUID:91148424; PMID:1997784
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A; Residues: 1-567 < MUN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASBEBTNLSKLVMKFWANFARNGNPNGEGLPHWPEYDQKEGYLQIGATTQQAQKLKGEEV
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A;Map position: 16q13-16q22.1
C;Superfamily: cholinesterase; cholinesterase homology
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; endoplasmic reticu
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-145/Domain: propeptide #status predicted <PRO>
F;50-553/Domain: cholinesterase homology <CHE>
F;146-567/Product: carboxylesterase #status experimental -
F;564-667/Region: endoplasmic reticulum retention signal #
F;221,468/Active site: Ser, His #status predicted
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Biochemistry 32, 11606-11617, 1993

A;Title: Glycosylation-dependent activity of baculovirus-expressed human A;Reference number: A48809; MUID:94032283; PMID:8218228

A;Accession: I61085
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R;Riddles, P.W.; Richards, L.J.; Bowles, M.R.; Pond, S.M.
Gene 108, 289-292, 1991
A;Title: Cloning and analysis of a cDNA encoding a human liver carboxylesterase.
A;Reference number: PS0280; MUID:92084150; PMID:1748313
A;Reference number: PS0280; MUID:92084150; PMID:1748313
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A;Residues: 1-17,'A',18-55,'G',57-535,'G',537-567 <KRO2>
A;Cross-references: GB:L07764; NID:g180947; PIDN:AAA16036.1;
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A;Residues: 1-55,'G',57-361,363-535,'G',537-567 <KRO1>
A;Cross-references: GB:L07765; NID:g180949; PIDN:AAA35711.1; PID:g180950
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A;Residues: 114'H',116-280,'A',282-300,'IGNSYLWTYRETQREST',318-336,'R',338-382,'GSPI',38
A;Cross-references: GB:M65261; NID:g187028; PIDN:AAA83932.1; PID:g187029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKG 249
LFLDLIADVMFGVPSVIVARNHRDAGAPTYMYEFQYRPSFSSDMKPKTVIGDHGDELFSV
                                                SILDLIGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFV
                                                                                                                                                                                                                                                                                                                                                                                  TLSOKTKSFT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLGPLRFTPPQPAEPWSFVKNATSYPPMCTQDPKAGQLLSELFTNRKENIPLKLSEDCLY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WLRAFILATISASAAWGH--PSSP-PVVDTVHGKVLGKFVSLEGFAQPVAIFLGIPFAKP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WCFFLILOPLLGHROWGKTGPSAEGPORNTRLGWIQGKOVTVLGSPVPVNVFLGVPFAAP 71
                                                                                                                                                      GWLI PMQLMSYPLSEGQLDQKTAMSLLWKSYPLVCIAKELIPEATEKYLGGTDDTVKKKD
                                                                                                                                                                                                                                                                                                         ETTLKMKFLSLDLQGDPRESQPLLGTVIDGMLLLKTPEELQAERNFHTVPYMVGINKQEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEHKAIMESGVAIIPYLEAHDYEK--SEDLQVVAHECGNNASDSEALLRCLRTKPSKELL 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STGDEHSRGNWGHLDQVAALRWVQDNIASFGGNPGSVTIFGESAGGESVSVLVLSPLAKN
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                                                                                                                                                                                                                            GFLLPMKEAPEILSGS--NKSLALHLIQN---ILHIPPQYLHLVANEYFHDKHSLTEIRD 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LFHRAISESGVALTSVLVKKGDVKPLAEQIAITA---
                                                                                                                                                                                                                                                                                                                                                                                  ----RVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHEC 352
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A;Residues: 1-6,'F',8-59,'P',61-212,'A',214-252,'T',254-309,'IT',312-341,'N',343-424,'FY
A;Rosidues: 1-6,'F',8-59,'P',61-212,'A',214-252,'T',254-309,'IT',312-341,'N',343-424,'FY
A;Note: the sequence in GenBank entry RNU10697, release 107, (PID:9562008) has the codon R;Robbi, M.; Beaufay, H.
submitted to the EMBL Data Library, September 1994
A;Reference number: S49257
A;Accession: S49257
                                                                                                                                                S
                                                                                                                                                                                                                                                                                                                                                 A;Description: catalyzes conversion of carboxylic ester to alcohol and carboxylic c;Superfamily: cholinesterase; cholinesterase homology C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Experimental source: liver R;Yan, B.; Yang, D.; Brady, M.; Parkinson, A. J. Biol. Chem. 269, 29688-29696, 1994
A;Title: Rat kidney carboxylesterase. Cloning, sequencing, A;Reference number: A55304; MUID:95050819; PMID:7961958
A;Accession: A55304
                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X81825; NID:g550417; PIDN:CAA57419.1; PID:g550418
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A; Residues: 1-561 < RO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Morgan, E.W.; Yan, B.; Greenway, D.; Petersen, D.R.; Parkinson, A. R;Morgan, E.W.; Yan, B.; Greenway, D.; Petersen, D.R.; Parkinson, A. Arch. Blochem. Biophys. 315, 495-512, 1994
A;Title: Purification and characterization of two rat liver microsomal carboxylesterases A;Reference number: S51202; MUID:95077430; PMID:7986098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1996 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S62788; S51203; A55304; S49257
R;Robbi, M.; van Schaftingen, E.; Beaufay, H.
Biochem. J. 313, 821-826, 1996
A;Title: Cloning and sequencing of rat liver carboxylesterase ES-4 (microsomal A;Reference number: S62788; MUID:96190723; PMID:8611161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q64573; EMBL:X81825; NID:g550417; PIDN:CAA57419.1; A;Experimental source: liver
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A; Residues: 1-561 < ROB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carboxylesterase (EC 3.1.1.1) ES-4 precursor,
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                                                                                                                                                                                                                                                             ;50-551/Domain: cholinesterase homology <CHE>;221,466/Active site: Ser, His #status predicted;301/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                   ;1-18/Domain: signal sequence #status predicted <SIG>;1-9-56//Product: carboxylesterase ES-4 #status experimental
                                                                                                                                                                                                                                                                                                                                                                                            Description: catalyzes conversion of carboxylic ester to alcohol
                                                                                                                                                                                              Matches
                                           62
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                                                                                                                                                                                                                Similarity
                                                                                                                                FLILOPLLGHROWGKTGPSAEGPORNTRLGWIQGKOVTVLGSPVPVNVFLGVPFAAPPLG 74
                                 STREAPPOPAREWSFVKNTTTYPPMCSQDAAKGQRMNDLLTNRKEKIH---LEFSEDCLY
                                                                       SLRFTNPQPASPWDNLREATSYPNLCLQNSEW-----LLLDQHMLKVHYPKFGVSEDCLY
                                                                                                           FLILVSLATCVVYG--NPSSP-PVVDTTKGKVLGKYVSLEGVTQSVAVFLGVPFAKPPLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GANTQAAQKLKDKEVAFWTN
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                                                                                                                                                                                            Conservative
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                                                                                                                                                                                    Score 1139; DB 2;
Pred. No. 1.5e-81;
2; Mismatches 195;
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LSWVQKWIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIPYLEA
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APILR-----DGASEEEIKLSKMVMKFWANFARNGNPNGRGLPHWPQYDQKEEYLQIGA 529
                                                                                                                                                                                            LDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFG
                                                                                                                                                                                                                                                                                                                     GAFLKGDIVMFEGATEEEKLLSRKOMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDL 529
                                                                                                                                                                                                                                                                       LLP--MKEAPEILSGSNKSLALHLIQ---NILHIPPQYLHLVANEYFHDKHSLTEIRDSL
TTQQSQRLKAEEVAFWTQLL
                                NMSLGQRLKEPRVDFWTSTI
                                                                                                                                                       LAFIGDVSFSIPSVMVSRDHRDAGAPTYMYEYQYYPSFSSPQRPKHVVGDHADDLYSVFG
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Carboxylesterase (EC 3.1.1.1) egasyn - mouse

N;Alternate names: beta-glucuronidase endoplasmic reticulum-targeting protein; esterase-;

C;Species: Mus musculus (house mouse)

C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004

C;Accession: A55281

R;Ovnic, M; Swank, R.T.; Fletcher, C.; Zhen, L.; Novak, E.K.; Baumann, H.; Heintz, N.; (
Genomics 11, 956-967, 1991

A;Title: Characterization and functional expression of a cDNA encoding egasyn (esterase-;
A;Reference number: A55281; MUID:92147141; PMID:1783403

A;Accession: A55281

A;Status: preliminary

A;Molecule type: mRNA; protein

A;Rolecule type: mRNA; protein

A;Rote: sequence extracted from NCBI backbone (NCBIN:80191, NCBIP:80194)

C;Superfamily: cholinesterase; cholinesterase homology

C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum

F;51-552/Domain: cholinesterase homology <CHE>

F;222,467/Active site: Ser, His #status predicted Local Similarity REATSYPNICLQNSEWILLDQHMLKVHYPKFGV--SEDCLYLNIYAPAHADTGSKLPVLV WIHGGGLVLGGASTYDGLVLSTHENVVVVVVIQYRLGIWGFFSTGDEHSRGNWGHLDQVAA KNATSYPPMCFODPVTGQIVNDLLTNRKEKIPLQFSEDCLYLNIYTPADLTKSDRLPVMV WFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAA 208 GHPSSPPMVDTVQGKVLGKYISLEGFTQPVAVFLGVPFAKPPLGSLRFAPPQPAEPWSSV Conservative 37.0%; 76; Score 1138.5; DB 2; Pred. No. 1.6e-81; 6; Mismatches 195; 2 Indels Length 29; Gaps 138 198 148 78

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A;Cross-reference
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P10959; GB:M20629; GB:X13587; NID:g203279; C;Superfamily: cholinesterase; cholinesterase homology C;Keywords: carboxylic ester hydrolase; glycoprotein P;1-9/Domain: signal sequence #status predicted <SIG-P;0-540/Product: carboxylesterase #status predicted <MAT-P;10-540/Product: carboxylesterase homology <CHE-P;41-529/Domain: cholinesterase homology <CHE-P;41-529/Domain: signal sequence #status predicted <MAT-P;212,444/Active site: Ser, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carboxylesterase (EC 3.1.1.1) precursor - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-May-1990 #sequence_revision 03-Aug-1992 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                      LAVCPIWGH----PSSP-PVVDTTKGKVLGKYVSLEGFTQPVAVFLGVPFAKPPLGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEVPTVLDGVLLPKMPEBILAEKNENTVPYIVGINKQEFGWILPTMMNYPPSDVKLDQMT 376
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                                            LSQK--TKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIGVNNHECGFLLPMKEAPEILS 366
                                                                               NLFHRAISESGVVLTTNLDKKNTQAV--AQMIATLSGCNNTSSAAMVQCLRQKTEAELLE
                                                                                                            GLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLT 308
                                                                                                                                                                 FTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAK 248
                                                                                                                                                                                                        LRFAPPEPAEPWSFVKNTTTYPPMCSQDGVVGKLLADMLSTGKESIPLEF----SEDCL
                                                                                                                                                                                                                                                                                                     LRFTNPQPASPWDNLREATSYPNLCLQN-----SEWILLDQHMLKVHYPKFGVSEDCL 128
                                                                                                                                                                                                                                                                                                                                                                  LILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAPPLGS
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                                                                                                                                           FSTGDEHSRGNWAHLDQLAALRWVQDNIANFGGNPDSVTIFGESAGGVSVSALVLSPLAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RDAGAPTYMYEFQYSPSFSSEMKPDTVVGDHGDEIYSVFGAPILRG-----GTSEEEIN
                  LTVKLDNTSMSTVIDGVVLPKTPEEILTEKSFNTVPYIVGFNKQEFGWIIPTMMGNLLSE
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                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 36.9%; Score 1136; DB 2;
43.3%; Pred. No. 2.4e-81;
ative 91; Mismatches 185;
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A;Experimental source: liver; endoplasmic reticulum C;Function:
A;Description: catalyzes conversion of carboxylic ester to alcohol and carboxylic anion C;Superfamily: cholinesterase; cholinesterase homology
C;Superfamily: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; liver
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-561/Product: carboxylesterase #status predicted <NAT>
F;50-551/Domain: cholinesterase homology <CHE>
F;50-551/Bomain: cholinesterase homology <CHE>
F;51-301/Bidding site: carbohydrate (Aan) (covalent) #status predicted
F;721.466/Active site: Ser, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Yan, B.; Yang, D.; Parkinson, A.
Arch. Biochem. Biophys. 317, 222-234, 1995
A;Title: Cloning and expression of hydrolase C, a member
A;Reference number: S71597; MUID:95177656; PMID:7872788
A;Accession: S71597
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%Alternate names: hydrolase C
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 13-Sep-1998
C;Accession: S71597
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A; Residues: 1-561 < YAN>
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  ESYHFLSTVIDDVVLPKDPKEILAEKNFNTVPYIVGINKQECGWLLPTMMRFVPPDVK-L
                                                                                                                                                                                                                                                                  VAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIPY
                                                                                                                                                                                                                                                                                                                                                                                VLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQ
                                                      S----FTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLP--MKEAPEILSGS
                                                                                                                                                     LEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQK------TK 314
                                                                                                                                                                                                                          VAALHWVQDNIANFGGDPGSVTIFGESAGGFSVSVLVLSPLSKNLYHRAISESGVVLITQ
                                                                                                                                                                                                                                                                                                                                    VMVWIHGGGLTQGGASTYDGRVLSAYENVVVVAIQYRLGIWGFFSTGDEHSRGNWGHLDQ
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                                                                                                                LFTKOVRPA--AKQIADMAĞCKTTTSAIIVHCLRQKTEBELLBIMBKMNLIKLSSQRDTK
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NKSLALHLIQ----NILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALIT

Db 171 RIGIWGFFSTGDEHRRGHUGGHLOVAALHWYDDIDRGGDDGSVTIFGESAGGESVSVL 230 Qy 242 ILSPMAKGLFHKAIMESGVALIPL-EAHDYEKSEDLOVVAHFCGNNASDSEALLRCLRT 300	Qy 73 LGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHMLKVHYPKF 121	Query Match 36.5%; Score 1123; DB 2; Length 561; Best Local Similarity 42.2%; Pred. No. 2.7e-80; Matches 245; Conservative 86; Mismatches 193; Indels 56; Gaps 11; Qy 13 CFFLILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAPP 72 : :	A; restautes: 503-554; R', 556-561 <med> A; Cross references: EMBL:X65295; NID:g57557; PIDN:CAA46390.1; PID:g57558 C; Superfamily: cholinesterase; cholinesterase homology C; Keywords: carboxylic ester hydrolase; glycoprotein F;1-18/Domain: signal sequence #status predicted <sig>F;1-9-561/Product: carboxylesterase ES-3 #status predicted <mat> F;50-551/Domain: cholinesterase homology <che> F;79,107,489/Binding site: carbohydrate (Asn) (covalent) #status predicted F;221,466/Active site: Ser, His #status predicted</che></mat></sig></med>	Eur. J. Biochem. 206, 801-806, 1992 A; Title: The carboxylesterase family exhibits C-terminal sequence diversity reflecting the A; Reference number: \$23460; MUID:92299008; PMID:1606962 A; Accession: \$23462 A; Status: preliminary; translation not shown A; Molecule type: mRNA	A;Title: Cloning and sequencing of rat liver carboxylesterase ES-3 (EGASYN). A;Reference number: JC2447; MUID:95032008; PMID:7945287 A;Accession: JC2447 A;Molecule type: mRNA A;Residues: 1-561 <rob> A;Residues: 1-561 <rob> A;Cross-references: UNIPROT:Q63108; GB:X81395; NID:g550146; PIDN:CAA57158.1; PID:g550147 A;Experimental source: liver R;Medda, S:; Proia, R.L.</rob></rob>	RESULT 14 JC2447 Carboxylesterase (EC 3.1.1.1) ES-3 precursor - rat C;Species: Rattus norvegious (Norway rat) C;Date: 29-Mar-1995 Hsequence_revision 26-May-1995 #text_change 09-Jul-2004 C;Accession: JC2447; S23462 R;Robbi, M.; Beaufay, H. BioChem. Bionhys Rea Commun 201 1404-1411 1864	Qy 546 TSTI 549 Db 546 TQLL 549	Db 372 DKKWAIMLLEKFASIYGIPEDIIFVAIEKYRKGSDDPIKIRDGILAFIGDVLECIPSVWV 431 Qy 426 ARYHRDAGAPVYFYEFRHRPQCFEDTKAPKYKADHADEVRFYFGAFLKGDIVMFEGATE 485
A; Molecule type: protein A; Molecule type: protein A; Residues: 19-26; 'D', 28-37 < GAU's C; Superfamily: cholinesterase; cholinesterase homology C; Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; homotrimer F; 1-18/Domain: signal sequence #status predicted <sig's #status="" (asn)="" (covalent)="" 19-565="" 50-551="" 79,489="" <che's="" <mat's="" binding="" carbohydrate="" carboxylesterase="" cholinesterase="" domain:="" f;="" homology="" predicted="" predicted<="" product:="" site:="" td=""><td></td><td>Reference number: \$51202; MUID:95077430; PMID:7986098 Accession: \$51202 Molecule type: protein Medda, S.; Prota, R.L. Medda, S.; Prota, R.L. Title: The carboxylesterase family exhibits C-terminal sequence dives Reference number: \$23460; MUID:92299008; PMID:1606962</td><td>submitted to the EMBL Data Library, February 1990 A;Reference number: \$12468 A;Reference number: \$12468 A;Rocession: \$12468 A;Molecule type: mRNA A;Residues: 1-264,'K',266-565 <rob2> A;Cross-references: EMBL.X51974; NID:956998; PIDN:CAA36236.1; PID:956899 R;Morgan, E.W.; Yan, B.; Greenway, D.; Petersen, D.R.; Parkinson, A. A;Title: Purification and characterization of two rat liver microsomal carboxylesterases</rob2></td><td>A; Accession: 51036/ A; Molecule type: mRNA A; Residues: 1-565 < ROB1> A; Cross-references: UNIPROT:Q9R135; EMBL:X51974 A; Note: 168-Gln, 247-Lys, 423-Met, and 506-Asn were also found A; Note: the sequence from Fig. 4 is inconsistent with that from Fig. 5 in having 265-Lys, R; Robbi, M.</td><td>names: hydrolase A attus norvegicus (Norway rat) un-1991 #sequence revision 30-Jun-1991 #text_cha S10367; S12468; \$51202; S23460; S14361 Beaufay, H.; Octave, J.N. Beaufay, H.; Octave, J.N. 269, 451-458, 1990 leotide sequence of cDNA coding for rat liver pI number: S10367; MUID:90351366; PMID:2386485</td><td>Db 522 EGYLQIGATTQQAQKLKEKEVAFWSELLAMKPLHA 556 RESULT 15 S10367 carboxylesterase (EC 3.1.1.1) ES-10 precursor, microsomal - rat</td><td>7 4 4 6 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2</td><td>Db 288 KTEEBLLETTIKINLFSLDIHGDSRQSYPFVPTVLDGVVLPKMPEEILAEKDFNTVPYIV 347 Qy 346 GVNNHECGFLLP-MKEAPEILSGSNKSLALHLIQNILHIPPQYLHLVANEYFHDKHS 401 Qj 348 GINKQEGGILPTMANYPPSDMKLDPMTATSLLKKSSFLLNLPEBAIFVAVEKYLRHTDD 407 Db 348 GINKQEGGILPTMANYPPSDMKLDPMTATSLLKKSSFLLNLPEBAIFVAVEKYLRHTDD 407 Qy 402 LTBIRDSLLDLLGDVFFVVPALITARYYHDGAPVYFYEFRHRPQCFEDTKPAFVKADH 461 </td></sig's>		Reference number: \$51202; MUID:95077430; PMID:7986098 Accession: \$51202 Molecule type: protein Medda, S.; Prota, R.L. Medda, S.; Prota, R.L. Title: The carboxylesterase family exhibits C-terminal sequence dives Reference number: \$23460; MUID:92299008; PMID:1606962	submitted to the EMBL Data Library, February 1990 A;Reference number: \$12468 A;Reference number: \$12468 A;Rocession: \$12468 A;Molecule type: mRNA A;Residues: 1-264,'K',266-565 <rob2> A;Cross-references: EMBL.X51974; NID:956998; PIDN:CAA36236.1; PID:956899 R;Morgan, E.W.; Yan, B.; Greenway, D.; Petersen, D.R.; Parkinson, A. A;Title: Purification and characterization of two rat liver microsomal carboxylesterases</rob2>	A; Accession: 51036/ A; Molecule type: mRNA A; Residues: 1-565 < ROB1> A; Cross-references: UNIPROT:Q9R135; EMBL:X51974 A; Note: 168-Gln, 247-Lys, 423-Met, and 506-Asn were also found A; Note: the sequence from Fig. 4 is inconsistent with that from Fig. 5 in having 265-Lys, R; Robbi, M.	names: hydrolase A attus norvegicus (Norway rat) un-1991 #sequence revision 30-Jun-1991 #text_cha S10367; S12468; \$51202; S23460; S14361 Beaufay, H.; Octave, J.N. Beaufay, H.; Octave, J.N. 269, 451-458, 1990 leotide sequence of cDNA coding for rat liver pI number: S10367; MUID:90351366; PMID:2386485	Db 522 EGYLQIGATTQQAQKLKEKEVAFWSELLAMKPLHA 556 RESULT 15 S10367 carboxylesterase (EC 3.1.1.1) ES-10 precursor, microsomal - rat	7 4 4 6 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Db 288 KTEEBLLETTIKINLFSLDIHGDSRQSYPFVPTVLDGVVLPKMPEEILAEKDFNTVPYIV 347 Qy 346 GVNNHECGFLLP-MKEAPEILSGSNKSLALHLIQNILHIPPQYLHLVANEYFHDKHS 401 Qj 348 GINKQEGGILPTMANYPPSDMKLDPMTATSLLKKSSFLLNLPEBAIFVAVEKYLRHTDD 407 Db 348 GINKQEGGILPTMANYPPSDMKLDPMTATSLLKKSSFLLNLPEBAIFVAVEKYLRHTDD 407 Qy 402 LTBIRDSLLDLLGDVFFVVPALITARYYHDGAPVYFYEFRHRPQCFEDTKPAFVKADH 461

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|:||:||:||:||:||:||:||
174 IWGFFSTGDEHSRGNWGHLDQVAALHWVQDNIANFGGNPGSVTIFGBSAGGFSVSALVLS 233
                                                                                                                                                                                                                                                                                                                                       471 FSVFGSPFLK-----DGASEETNLSKWVMKYWANFARNGSPNGGGLPHWPEYDQKEGY 524
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LKIGASTQAAQRLKDKEVAFWSE----LRAKEAAEEP 557
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Minimum DB seq length: 0
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
/ Cgm2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*
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/ Cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/ Cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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 Sequence 2, Appli	Sequence 2219, Ap	Sequence 2, Appli	Sequence 196, App	Sequence 2375, Ap	Sequence 92, Appl	Sequence 10, Appl	Sequence 91, Appl	Sequence 46, Appl	Sequence 2, Appli	Sequence 2, Appli	Description

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ALIGNMENTS

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APPLICANT: CAUTLIS, ROTY A. J.
APPLICANT: Silos-Santiago, Inmaculada
FIITLB OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-122001
CURRENT APPLICATION NUMBER: US/10/023,515
CURRENT FILING DATE: 2001-12-18
FRIOR APPLICATION NUMBER: 60/256,369
PRIOR FILING DATE: 2000-12-18
FRIOR APPLICATION NUMBER: 60/279,508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LENGTH: 581
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-515-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10023515; Publication No. US20020182636A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-023-515-2
                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 3079; DB 13; Length 581; Best Local Similarity 100.0%; Pred. No. 1.1e-277; Matches 581; Conservative 0; Mismatches 0; Indels 0;
61 NVFLGVPFAAPPLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLLDQHMLKVHYPK 120
                                                                                                                                             0; Indels 0;
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APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERA
TITLE OF INVENTION: 53011, M MOVEL HUMAN CARBOXYLESTERA
TITLE OF INVENTION: PAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-122001
CURRENT APPLICATION NUMBER: US/10/674,636
CURRENT APPLICATION NUMBER: US/10/023,515
FRIOR APPLICATION NUMBER: US/10/023,515
FRIOR APPLICATION NUMBER: 60/256,369
FRIOR APPLICATION NUMBER: 60/279,508
FRIOR APPLICATION NUMBER: 60/279,508
FRIOR FILING DATE: 2000-12-18
FRIOR APPLICATION NUMBER: 60/279,508
FRIOR APPLICATION NUMBER: 60/279,508
FRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 581
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-674-636-2
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Best Local S
Matches 581
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Publication No. US20040086922A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                       581;
                 61 NVFLGVÞFAAPÞLGSLRFTNÞQÞASÞWDNLREATSVÞNLCLQNSEWLLLDQHMLKVHYÞK
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                                                                                    1 MPQGLTSSASQWCFFLILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPV
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                                                                                                                                                         Similarity
MPQGLTSSASQWCFFLILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVDFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFFCAP
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                                                                                                                                       Conservative
                                                                                                                                                     100.0%;
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                                                                                                                                   Score 3079; DB 15;
Pred. No. 1.1e-277;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN CARBOXYLESTERASE
                                                                                                                                     Indels
                                                                                                                                                                   Length
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밁 ঠ 유왕

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APPLICANT: KAICHCEL, Venkateswarlu

APPLICANT: KSIJOS-Santiago, Inmaculada

APPLICANT: SIJOS-Santiago, Inmaculada

APPLICANT: SIJAS-Santiago, Santiago, 54181, 211, 5687, 884,

ITILE DE INVENTION: MCHOCGICAL DISORDERS USING 44390, 54181, 211, 5687, 2047,

ITILE DE INVENTION: 33751, 52872, 14063, 20739, 32544, 42239, 4373, 51164,

ITILE DE INVENTION: 33751, 52872, 14063, 20739, 32520, 5296, 69112, 14990,

ITILE DE INVENTION: 33751, 52872, 14063, 2073, 32620, 5277, 619, 1423,

ITILE DE INVENTION: 18547, 115, 579, 15985, 15625, 766, 18603, 2395, 2554, 8675,

ITILE DE INVENTION: 12549, 8626, 13231, 30209, 577, 619, 1423,

ITILE DE INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR

ITILE DE INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR

ITILE DE INVENTION: 2004-01-14

PRICE REPEBRUCE: MPIO3-007PIRNOMIN

CURRENT FILING DATE: 2003-01-15

PRICE REPLICATION NUMBER: US 60/440,318

PRICE PILING DATE: 2003-03-07-18

PRICE REPLICATION NUMBER: US 60/447,83

PRICE PILING DATE: 2003-05-08

PRICE REPLICATION NUMBER: US 60/457,901

PRICE PILING DATE: 2003-05-19

PRICE PILING DATE: 2003-07-18

PRICE PILING DATE: 2003-07-1
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Publication No. US20040197825A1
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APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM p.l.c.
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50039
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/US01/49232
PRIOR PILING DATE: 2000-12-17
PRIOR PILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR PILING DATE: 2000-12-0
PRIOR APPLICATION NUMBER: 60/260,482
                                                                                                                                                                                                                       RESULT 4
US-10-451-168-91
Sequence 91, Application US/10451168
Publication No. US20040091969A1
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-10-757-262-46
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Pred. No. 1.1e-277;
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PRIOR APPLICATION NUMBER: 60/264,922
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR FILING DATE: 2001-04-04
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/289,622
PRIOR FILING DATE: 2002-06-28
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LENGTH: 575
TYPE: PRT
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Best Local
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WDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPWAKGLF
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                                                                         RKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIPL
                                                                                                                                AGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEBEKLLS
                                                                                                                                                                                        LALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRD
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                                                       RKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIPL
                                                                                                                                                                        LALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRD
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Pred. No. 2.1e-262;
3; Mismatches 6;
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Sequence 10, Application US/10433256
Publication No. US20040081980A1
GENERAL INFORMATION:
APPLICANT: SANJANWALA, Madhusudan M.; YAO, Monique
APPLICANT: AU-YOUNG, Janice K.; BAUGHN, Mariah R.
APPLICANT: AVIZU, Chandra S.; RING, Huijun Z.
APPLICANT: LEE, Ernestine A.; DING, Li

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RESULT 5 US-10-433-256-10

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APPLICANT: HAFALIA, April J.A.; TANG, Y. Tom APPLICANT: VUE, Henry; TRIBOULEY, Catherine M. APPLICANT: LU, Dyung Aina M.; LAL, Preeti G. APPLICANT: WARREN, Bridget A.; YANG, Jumming APPLICANT: CHAWLA, Narinder K.; NGUYEN, Danniel APPLICANT: GANUHI, Ameena R.; LU, Yan APPLICANT: ISON, Crealg H.

TITLE OF INVENTION: DRUG METABOLIZING ENZYMES FILE REFERENCE: PI-0313 USN
CURRENT APPLICATION NUMBER: US/10/433,256
CURRENT PILING DATE: 2003-05-30
PRIOR APPLICATION NUMBER: PCT/US01/47429
PRIOR APPLICATION NUMBER: PCT/US01/47429
PRIOR APPLICATION NUMBER: US 60/254,308
PRIOR APPLICATION NUMBER: US 60/254,308
PRIOR APPLICATION NUMBER: US 60/256,189
PRIOR APPLICATION NUMBER: US 60/257,713
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 60/257,713
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 60/262,706
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/266,020
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-02
SOPTWARE: PERL PROGram
SEQ ID NO 10
LENGTH: 642
TYPE: PRT
CREANISM: Homo samiang
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FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 6538080CD1
US-10-433-256-10
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Best Local Similarity
Matches 548; Conserv
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               DLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIPLILSASDMLHSPLSSLTFLS 570
                                                                                           TKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMKXWATFARTGNENGN
                                                                                                                                                                    VANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFED
                                                                                                                                            VANEYFIDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFED
                                                                                                                                                                                                                                            DLLSQKAFKAIPSIIGVNNHECGFLLPMKEAPEILSGSNKSLALHLIQNILHIPPQYLHL 390
                                                                                                                                                                                                                                                                                                                        WVGKNIEFFGGDFSSVTIFGESAGAISVSSLILSEMAKGLFHKAIMESGVAIIPYLEAHD
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YUE, Henry; TRIBOUIEY, Catherine M.
LU, Dyung Aina M.; LAL, Preeti G.
WARREN, Bridget A.; YANG, Junming
CHAWLA, Narinder K.; NGUYEN, Danniel B.
GANDHI, Ameena R.; LU, Yan
ISON, Craig H.
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ilarity 99.5%;
Conservative
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Pred. No. 6.3e-261;
2; Mismatches 1;
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CURRENT APPLICATION NUMBER: US/10/451,168

CURRENT PILING DATE: 2003-11-12

PRIOR APPLICATION NUMBER: EC/US01/49232

PRIOR FILING DATE: 2000-12-17

PRIOR FILING DATE: 2000-12-17

PRIOR APPLICATION NUMBER: 60/256,710

PRIOR APPLICATION NUMBER: 60/257,048

PRIOR APPLICATION NUMBER: 60/260,482

PRIOR FILING DATE: 2000-12-20

PRIOR FILING DATE: 2001-01-09

PRIOR APPLICATION NUMBER: 60/264,922

PRIOR APPLICATION NUMBER: 60/264,922

PRIOR APPLICATION NUMBER: 60/266,797

PRIOR APPLICATION NUMBER: 60/266,797

PRIOR FILING DATE: 2001-03-06

PRIOR FILING DATE: 2001-03-19

PRIOR APPLICATION NUMBER: 60/266,797

PRIOR APPLICATION NUMBER: 60/266,797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 92, Application US/10451168 ; Publication No. US20040091969A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-451-168-92
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PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FRETSEQ for Windows Version
SEQ ID NO 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: NOVEL COMPOUNDS
                                                                                                                                          252
                                                                                                                                                                                                                                                    186
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KSLAL-----HLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALI
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                                                                                                                                                                      HKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSBALLRCLRTKDSKELLTLSQ 311
                                                                                                                                                                                                                                       WDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLF 251
                                                                                                                                                                                                                                                                                                                                    TYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQVRLGIFGFFTT 185
                                                                                                                                                                                                                                                                                                                                                                IYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTT 191
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                                             KTKSFTRVVDGAFFENEPLDLLSQKAFKAIPSIIGVNNHECGFLLEMVRILAVHTATPSN 365
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APPLICANT: SEKI, NACHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: MAGNIKO, YASUHIKO
ITILE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver: 2:1
SEQ ID NO 2375
LENGTH: 525
TYEE: PRT
ORGANISM: Homo sapiens
US-10-094-749-2375
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Best Local Similarity 90.9%;
Matches 501; Conservative
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Sequence 2375, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ISOGAI, 'APPLICANT: SUGIYAM APPLICANT: OTSUKI, APPLICANT: WAKAMAT
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NAGAI, KEIICHI
IRIE, RYOTARO
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OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
                                                                                                                                   REATSYPNICLQNSEWILLDQHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWF 150
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WVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIFYLEAHD
                                                                                                             REATSYPHICLONSEWILLIDOHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKIPVLVWF
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                                                                    PGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALS
                                                 PGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALS
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                                                                                                                                                                                                                                        Score 2606; DB 15;
Pred. No. 1.2e-233;
0; Mismatches 0;
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US-10-114-270-196
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              CURRENT APPLICATION NUMBER: US/10/114,270
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/281,086
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR APPLICATION NUMBER: 60/281,863
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-04-05
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APPLICANT:
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APPLICANT:
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APPLICANT: Rothenberg, Mark E.
TITLE OF INVENTION: No. US20040030110A1el Proteins and Nucleic Acids
FILE REFERENCE: 21402-322C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
    APPLICATION NUMBER: 60/281,906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Guo, Xiaojia
: Kekuda, Ramesh
: Miller, Charles E.
: Malyankar, Uriel M.
: Spytek, Kimberly A.
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                                                                                                                                                                                                                                                                                                    Taupier Jr., Raymond J. Casman, Stacie J.
                                                                                                                                                                                                                                                                                                                                      Padigaru, Muralidhara
Shimkets, Richard A.
Gangolli, Esha A.
                                                                                                                                                                                                                                                                                                                                                                                      Smithson, Glennda
Burgess, Catherine E.
Gerlach, Valerie
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Gorman, Linda
Shenoy, Suresh G.
                                                                                                                                                                                                            Stone, David J.
                                                                                                                                                                                                                                        Rastelli, Luca
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pena,
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                                                                                                                                                                                                                         Edinger, Shlomit R.
                                                                                                                                                                                                                                                                                       Ji, Weizhen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vernet, Corine
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                                                                                                                                                                                                                                                                          Anderson, David W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vladimir Y.
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Same

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RESULT 9
US-10-381-898-2
US-10-381-898-2
Sequence 2, Application US/10381898
Publication No. US20040086887A1
GENERAL INFORMATION:
APPLICANT: AZIMZAI, Yalda, BAUGHN, Mariah R.;
APPLICANT: BOROMSKY, Mark L.; DING, Li;
APPLICANT: BOROMSKY, Mark LLIOTT, Vicki S.;
APPLICANT: DUGGAN, Brendan; ELLIOTT, Vicki S.;
APPLICANT: GAUDHI, Ameena R.; GRIFFIN, Jennifer A.;
APPLICANT: HAFALIA, April J.A.; ISON, Craig H.;
KHAN, Farrah A.; LAL, Preeti G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,020
; PRIOR APPLICATION NUMBER: 60/282,930
; PRIOR APPLICATION NUMBER: 60/282,930
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR APPLICATION NUMBER: 60/283,512
PRIOR FILING DATE: 2001-04-12
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283,710
PRIOR APPLICATION NUMBER: 60/283,710
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Pred. No. 8.7e-233;
4; Mismatches 17; I.
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APPLICANT: LEE, Ernestine A.; LU, Dyung Ain:
APPLICANT: ARVIZU, Chandra S.; POLICKY, Jen:
APPLICANT: RAMKUMAR, Jayalaxmi; RIMG, Huiju:
APPLICANT: TANG, Y. Tom; TRIBOULEY, Catheri:
APPLICANT: TANG, Y. Tom; TRIBOULEY, Catheri:
APPLICANT: TANG, Y. Tom; TRIBOULEY, Catheri:
APPLICANT: YANG, Bridget; XU, Yuming;
APPLICANT: YANG, Junming; YAO, Monique; YUE
ITILE OF INVENTION: DRUG METABOLIZING ENZYME.
FILE REFERENCE: PI-0233 USN
CURRENT APPLICATION NUMBER: US/10/381,898
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: PCT/US01/30662
PRIOR APPLICATION NUMBER: US 60/236,947
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: US 60/236,947
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/242,323
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/247,581
PRIOR APPLICATION NUMBER: US 60/247,581
PRIOR APPLICATION NUMBER: US 60/249,519
PRIOR APPLICATION NUMBER: US 60/249,519
PRIOR APPLICATION NUMBER: US 60/252,834
PRIOR FILING DATE: 2000-11-16
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/252,834
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/252,834
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/252,834
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/252,834
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEG ID NOS: 36
SOFTWARE: PERL PROGram
SEG ID NO 2
LENGTH: 618
TYPE: PRT
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Best Local 9
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No
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Similarity 94.4%;
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ARVIZU, Chandra S.; POLICKY, Jennifer L.;
RAMKUMAR, Jayalaxmi; RING, Huijun Z.;
SANJANWALA, Madhusudan M.;
TANG, Y. Tom; TRIBOULBY, Catherine M.;
CHAWLA, Narinder K.; WALSH, Roderick T.;
WARREN, Bridget; XU, Yuming;
YANG, Junming; YAO, Monique; YUE, Henry
INVENTION: DRUG METABOLIZING ENZYMES
TKPAFYKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKOMKYWATFARTGNPNGN
                                                                     DLLSQKAFKAIPSIIGVNNHECGFLLPMKEAPEILSGSNKSLALHLIQNILHIPPQYLHL
                                                                                                                                                                                                                                                                             YEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEPL 330
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Pred. No. 6.6e
1; Mismatches
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.6e-232;
es 5; Indels
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RESULT 11
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US-10-104-047-2219
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Sequence 2, Application US/10233933A
Publication No. US20040214171A1
GENERAL INFORMATION:
APPLICANT: Yamashita, Tetsuro
APPLICANT: Miyazaki, Masao
TITLE OF INVENTION: CAT KIDNEY
PILE REFERENCE: SHIG PP02US006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOPTWARE: PatentIn Ver.
SEQ ID NO 2219
LENGTH: 469
TYPE: PRT
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TITLE OF INVENTION: NO. US20030236392A1e1 full length
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
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Local Similarity 99.6%;
hes 467; Conservative
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                                                                                                                                                                                                                                                                                         LGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAF
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Pred. No. 1.5e-219;
2; Mismatches 0;
                DISEASE MARKER
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; LENGTH: 542
; TYPE: PRT
; ORGANISM: Felis c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                           GDERKKDLQVLARICGCHASDSAALLQCLRAKPSEELMDISKKLTFSIPVIDDFFFFDEP
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                                                                                                                                    LVANEYFHDKHSLTBIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFE
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                                                                                                                                                                                      DYEKSEDLOVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEP
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; Pred. No. 1e-175; 
60; Mismatches 85;
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RESULT 12
US-10-233-933A-4
; Sequence 4, Application US/10233933A
; Publication No. US20040214171A1
; GENERAL INFORMATION:
; APPLICANT: Yamashita, Tetsuro
; APPLICANT: Miyazaki, Masao
; TITLS OF INVENTION: CAT KIDNEY DISEASE MARKER
; FILE REFERENCE: SHIG FP02US006
; CURRENT APPLICATION NUMBER: US/10/233,933A
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: JP2002-057908
; PRIOR FILING DATE: 2002-04-03
; MUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO
; SEQ ID NO
; SEQ ID NO
; SEQ ID NO
; TYPE: PRT
; ORGANISM: Felis catus
US-10-233-933A-4

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CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/US01/49232
PRIOR FILING DATE: 2000-12-17
PRIOR PELLOATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR APPLICATION NUMBER: 60/250,482
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-03-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-451-168-93
; Sequence 93, Application US/10451168
; Publication No. US20040091969A1
; GENERAL INFORMATION:
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Best Local Similarity
Matches 373; Conserv
   NUMBER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SMITHKLINE BEECHAM CORPORATION APPLICANT: SMITHKLINE BEECHAM p.l.c.
                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL COMPOUNDS
               FILING DATE: 2001-04-04
APPLICATION NUMBER: 60/289,622
FILING DATE: 2002-06-28
                                                                     APPLICATION NUMBER: 60/281,535
                                                                                           FILING DATE: 2001-03-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWATFARTGNPNG 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFE 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDLLSQKAFKAIPSIIGVNNHECGFLLPMKEAPEILSGSNKSLALHLIQNILHIPPQYLH 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDERKKDLQVLARICGCHASDSAALLQCLRAKPSEELMDISKKLTFSIPVIDDFFFPDEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPAADAPVRSTRLGWVRGKQTTVLGSTVPVNMFLGIPYAAPPLGFLRFKQPKPALPGNDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WVRDNIEFFGGDPRSVTIFGESAGAISVSSLILSPIANGLFHKAIMESGVAILPLLMRPP 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGGAFKMGSASSFDGSALAAYEDVLIVTTQYRLGIFGFFDTGDEHARGNWALLDQVAALT
                                                                                                                                                                                                                                                                                                                                                                                                                                     GLAXO GROUP LIMITED
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMITHKLINE BEECHAM p.1.c.
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NOS:
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (1)
OTHER INFORMATION: Xaa equals an
NAME/KEY: SITE
LOCATION: (7)
COTHER INFORMATION: Xaa equals an
US-09-925-298-689
                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: ROSEN et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PAIO3

CURRENT APPLICATION NUMBER: US/09/925,298

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05881

PRIOR APPLICATION NUMBER: PCT/US00/05881

PRIOR APPLICATION NUMBER: D0/124,270

PRIOR FILING DATE: 1909-03-12

NUMBER OF SEQ ID NOS: 846

SOPTWARE: Patentin Ver. 2.0

SEQ ID NO 689

FENORH: 549

TUNDER DATE: 1999-03-12
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US-09-925-298-689
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Best Local S
Matches 248
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; SEQ ID NO 93
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-451-168-93
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Best Local
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                                                                   248;
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                                                                                 Similarity
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 GQDSASPIRTTHTGQVLGSLVHVKGANAGVQTFLGIPFAKPPLGPLRFAPPEPPESWSGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATEEEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09925298
o. US20020039764A1
                                                              39.9%; Score 1230; I ilarity 46.7%; Pred. No. 2.66 Conservative 91; Mismatches
                                                                                                                                               Xaa equals any of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1780; DB L5; Pred. No. 7.1e-157;
                                                                                                                                                                                                any of the naturally occurring
                                                                0; DB 9;
2.6e-105;
ches 168;
                                                                                                                                            naturally occurring L-amino acids
                                                                                             Length 549;
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NAME/KEY: SITE

LOCATION: (1)

TOTHER INFORMATION: Xaa equals any of the naturally occurring L-amino NAME/KEY: SITE

LOCATION: (7)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino US-10-102-806-689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-10-102-806-689
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                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 689, Application US/10102806 Publication No. US20030054421A1 GENERAL INFORMATION:
                                                                                           Query Match 39.9%; Score 1230; DB 14; Best Local Similarity 46.7%; Pred. No. 2.6e-105; Matches 248; Conservative 91; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 846
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA103P1C1
                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo
                                                                                                                                                                                                                                                                            PEATURE:
                                                                                                                                                                                                                                                                                                                             ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308
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                                                    31 GPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAPPLGSLRFTNPQPASPWDNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAALRWYQQNIAHFGGNPDRVTIFGESAGGTSVSSLVVSPISQGLFHGAIMESGVALLPG
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                              GQDSASPIRTTHTGQVLGSLVHVKGANAGVQTFLGIPFAKPPLGPLRFAPPEPPESWSGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPQHQPSWLKNIRPPHMKADHGDELPFVF-RSFFGGNYIKF---TBEEEQLSRKMMKYWA
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REATSYPNLCLQN-----SEWLLLDQHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFY
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                                                     EFQHQPSWLKNIRPPHMKADHGDELPFVF-RSFFGGNYIKF---TEEEEQLSRKWMKYWA
                                                                            EFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWA 499
                                                                                                              LIMIPPTFGDLLREBYIGDNGDPQTLQAQFQEWMADSMFVIPALQVAHF-QCSRAPVYFY
                                                                                                                                          ILHIPPQYLHLVANEYFHDKHSLTBIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFY
                                                                                                                                                                       FLPRHPQELLASADFQPVPSIVGVNNNEFGWLIPKVWRIYDTQKEMDREASQAALQKMLT
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Search completed: June 15, 2005, 09:46:09 Job time: 88 secs

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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
-Q-/cgm2 1/USFTO spool/6664091/runat 14062005 133640 10451/app_query.fasta 1.775
-DB=N Geneseq 16Dec04 -OPMT=fastap -SUPFIX=p2n.rng -MIMMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN-0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -NINLEN=0 -MAXLEN=200000000
-USER=6664091 @CGN 1 1 470 @PUNAT 14062005 133640 10451 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Listing first 45 summaries
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Abx89411 DNA encod	Aca03873 cDNA enco	10 Human	Abl95693 Human ang	Abl88204 Human PRO	3640	Aas21514 Human cDN	Aaa96341 cDNA enco	Aad08405 Human sec	Ads10162 Human the	Aad00680 Human Hyd	87 cDNA	Aad24096 Human car	4053 CES2 1	Abx71401 Human met	w	Abt40829 Toxicity	•	28	3 Rat sec	4 Human	_	Gene #	Breast	Abl62492 Colon ade	Color	CES2 1	CES2		-	z	3 Hum	Nove]	Adf50144 Cat cauxi	Cat		267 H	68 Humar	170 Novel h	Adb62095 Human cDN

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present nucleotide sequence, the coding region of which is also CC claimed, is that of cDNA encoding human 53010, a novel member of the CC carboxylesterase family. The invention provides 53010 nucleic acids, CC antisense molecules, expression vectors, host cells, transgenic animals, CC 53010 proteins, fusion proteins, antigenic peptides, anti-53010 CC antibodies and methods for detecting the presence of 53010 polypeptides cor nucleic acids, of identifying a compound that binds to the 53010 CC polypeptide, and of modulating the activity of the polypeptide. The 53010 CC polypeptide, and of modulating the activity of the polypeptide. The 53010 CC polypeptide, and polypeptides can act as novel diagnostic and CC therapeutic agents for controlling disorders involving aberrant or CC deficient hydrolysis of carboxylic esters. As 53010 molecules can cc expression is regulated in some rodent pain models, 53010 molecules can also act as novel diagnostic targets and therapeutic agents for CC controlling neurological disorders, such as pain-related disorders. A CC claimed method of treating or preventing a disorder (especially a pain-clated disorder) characterised by aberrant activity of a 53010 cc expression. 53010 mucleic acids are also useful in chromosome mapping, tissue typing, in forensic biology, prognostic assays, in CC and in obharmacoenomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2158
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28-MAR-2001; 2001US-0279508P.
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                                         ProGlnProAlaSerProTrpAspAsnLeuArgGluAlaThrSerTyrProAsnLeuCys
                                                                                                                                                                               ThrArgLeuGlyTrpIleGlnGlyLysGlnValThrValLeuGlySerProValProVal
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08-MAY-2003;
19-MAY-2003;
16-JUN-2003;
16-JUL-2003;
30-JUL-2003;
26-SEP-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          urological disorder; uropathic; cytostatic; urinary incontinence; benign prostatic hyperplasia; human; gene; ss.
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Use of polypeptides related to urological disorders, e.g. 44390, 5 211 or for identifying a compound capable of treating a urological
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disorder or identifying and treating a subject having a urological disorder.

The present invention describes the use of polypeptides related to compound capable of treating a urological disorder. Also described: (1) a method for identifying a compound capable of treating a urological compound capable of treating a urological compound capable of treating a urological compound; (2) a method for identifying a subject having a urological compound capable of treating a subject having a urological compound capable of urological disorders are useful for identifying a compound capable of treating a urological disorder, identifying a compound capable of treating a urological disorder, identifying a urological disorder. Disorders include urinary incontinence and benign prostatic compound capable of treating a urological disorder compound. The present sequence encodes a human urological disorder compound capable of treating a urological disorder compound. The present sequence encodes a human urological disorder compound prostation is used in the exemplification of the present

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AACGTGTTCCTCGGAGTCCCCCTTTGCTGCTCCCCCGCTGGGATCCCTGCGATTTACGAAC AsnValPheLeuGlyValProPheAlaAlaProProLeuGlySerLeuArgPheThrAsn ThrArgLeuGlyTrpIleGlnGlyLygGlnValThrValLeuGlySerProValProVal ACCAGGCTGGGATGGATTCAGGGCAAGCAAGTCACTGTGCTGGGAAGCCCCTGTGCCTGTG 80 335 275 60

CCGCAGCCTGCATCGCCCTGGGATAACTTGCGAGAAGCCACCTCCTACCCTAATTTGTGC ProGlnProAlaSerProTrpAspAsnLeuArgGluAlaThrSerTyrProAsnLeuCys 100 395

CTCCAGAACTCAGAGTGGCTGCTCTTAGATCAACACATGCTCAAGGTGCATTACCCGAAA LeuGlnAsnSerGluTrpLeuLeuLeuAspGlnHisMetLeuLysValHisTyrProLys 455 120

PheGlyValSerGluAspCysLeuTyrLeuAsnIleTyrAlaProAlaHisAlaAspThr TTCGGAGTGTCAGAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCACGCCGATACA 140 515

GlySerLysLeuProValLeuValTrpPheProGlyGlyAlaPheLysThrGlySerAla 160 GGCTCCAAGCTCCCCGTCTTGGTGTGGTTCCCCAGGAGGTGCCTTCAAGACTGGCTCAGCC 575

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                                                  ArgValAspPheTrpThrSerThrIleProLeuIleLeuSerAlaSerAspMetLeuHis
                                                                                                         ThrGluGlnTyrLeuGlnLeuAspLeuAsnMetSerLeuGlyGlnArgLeuLysGluPro 540
                             CGGGTGGATTTTTGGACCAGCACCATCCCCCTGATCCTGTCTGCCTCCGACATGCTCCAC
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The invention relates to an isolated polypeptide with signal sequences which allow it to be secreted extracellularly or membrane associated. T activity of polypeptides of the invention may be described as, cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropineuroprotective, immunosuppressive, haemostatic, antiinflammatory, cardiant, antiulcer, virucide, antithyroid, cerebroprotective, anorecti

nootropic, anorectic

The

Claim

2(a); Page

335pp;

English

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KW Human; cytostatic; vulnerary; antiarteriosclerotic; antiparkinsonian; KW mootropic; neuroprotective; immunosuppressive; haemostatic; KW mootropic; neuroprotective; immunosuppressive; haemostatic; KW cerebroprotective; cardiant; antiulcer; virucide; antithyroid; KW wound healing disorders; atherosclerosis; Parkinson's disease; KW wound healing disorders; atherosclerosis; Parkinson's disease; infection; KW wound healing disorders; atherosclerosis; parkinson's disease; hipterioristic disorder; kW inflammation; neoplastic disease; nervous system disorder; KW cardiovascular disorders; pancreatitis; respiratory disorder; KW hyperproliferation; systemic autoimmune disease; hyper-immunity; KW developmental abnormality; gastrointestinal ulceration; neuropathy; KW haematological disease; metabolic disease; sprem dysfunction; thyroid disorder; hypothyroidism; brain damage; colitis; KW cone photo- transduction deficiency; neurological disease; stroke; angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart; KW trachea; thymus; lymph node; muscular system; obesity; anorexia; KW growth abnormality; precocious puberty; gene; ss.
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20-DEC-2000; 2000US-0257048P.
09-JAN-2001; 2001US-0264922P.
30-JAN-2001; 2001US-0264922P.
06-FEB-2001; 2001US-0266797P.
19-MAR-2001; 2001US-0276988P.
04-APR-2001; 2001US-0289522P.
                                                                                                              Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder
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Best Local Similarity:
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                                                                            IleLeuSerAlaSerAspMetLeuHisSerProLeuSerSerLeuThrPheLeuSerLeu
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The invention relates to an isolated human drug metabolising enzyme (DME) and its nucleotide. DME is useful for diagnosing, treating or preventing disorders associated with aberrant expression of DME, where the disorders immunodeficiency syndrome (AIDS), asthma, atherosclerosis, psoriasis, cirrhosis, hepatitis, and cancer; a neurological disorder such as acquired nyelisis, a cell proliferative disorder such as arteriosclerosis, cirrhosis, hepatitis, and cancer; a neurological disorder such as Alaheimer's disease, Huntington's disease, dementia, parkinson's disease, aneemia; an endocrine disorder such as renal tubular acidosis, epilepsy, anaemia; an endocrine disorder such as adenoma, thrombosis and infections; an eye disorder such as conjunctivitis, glaucoma, cataract; metabolic disorder such as conjunctivitis, glaucoma, cataract; metabolic disorder such as cystic fibrosis, diabetes and goitre; a gastrointestinal
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15-DEC-2000;
21-DEC-2000;
19-JAN-2001;
                                                                                                                                                                                                                                                  Novel human drug metabolizing polypeptide, useful in diagnosis, prevention or treatment of autoimmune/inflammatory, cell proliferative, neurological, developmental, endocrine, metabolic and gastrointestinal
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Warren BA,
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.a AJA, Tang YT, Yue H, Tribouley
.g J, Walia NK, Nguyen DB, Gandhi
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                                                                                                                                                                                                                                                                                                                                                                                   used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorders, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp polymucleotide of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIFO at www.wipo.int/pct/en/sequences/listing.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
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New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.

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Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                     WPI; 2003-450961/43.
P-PSDB; ADB64065.
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25-JAN-2002;
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Hio Y, Otsuka K, Nagai
Otsuka M, Nagahari K, N
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                                       The invention discloses a polynucleotide comprising a sequence selected CC from 1970 fully defined nucleotide sequences which encode novel CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide CC or its partial peptide, an antibody binding to the polypeptide or peptide or the polynucleotide, immunologically assaying the polypeptide or peptide or peptide of the polynucleotide by contacting the polypeptide or peptide CC with the antibody of the encoded protein, and observing the binding CC between the two, a transformant carrying the polynucleotide in an CC expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide, or as a probe CC for detecting the polynucleotide. The polynucleotide coded CC proteins are useful as pharmaceutical agents and many disease-related CC genes may be included in them, for developing a diagnostic marker or CC medicines for regulation of their expression and activity, or as targets CC regeneration. Membrane proteins, signal transduction-related proteins, concer, tumours for diseases (e.g. osteoporosis, curvalogical diseases, cancer, tumours The CDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The Sequence presented is a cDNA of the invention. Note: Some of the sequence code data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
2092 BP;
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464 A; 552 C; 497 G; 579 T; 0 U; 0 Other;
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Percent Similarity:
Best Local Similarity:
Query Match: 7e-263 2877.00 98.40% 98.04% 93.44% Length:
Matches:
Conservative:
Mismatches:
Indels: 2092 551 2 2 7 2

밁 र् 밁 8 8 ঠ B ঠ US-10-023-515-2 (1-581) x ADB62095 (1-2092) 237 177 126 CACTITAACTGG-----84 64 44 24 HisargGlnTrpGlyLysThrGlyProSerAlaGluGlyProGlnArgAsnThrArgLeu LeuGlyValProPheAlaAlaProProLeuGlySerLeuArgPheThrAsnProGlnPro GlyTrpIleGlnGlyLysGlnValThrValLeuGlySerProValProValAsnValPhe AlaSerProTrpAspAsnLeuArgGluAlaThrSerTyrProAsnLeu------Cy GGATGGATTCAGGGCAAGCAAGTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTC CTCGGAGTCCCCTTTGCTGCTCCCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCT Gaps: 296 83 176 236 63

nTyrargLeuGlyIlePheGlyPhePheThrThrTrpAspGlnHisAlaProGlyAsnTr aSerIlePheAspGlySerAlaLeuAlaAlaTyrGluAspValLeuValValValValGl sPheGlyValSerGluAspCysLeuTyrLeuAsnIleTyrAlaProAlaHisAlaAspTh sLeuGlnAsnSerGluTrpLeuLeuLeuAspGlnHisMetLeuLysValHisTyrProLy rGlySerLysLeuProValLeuValTrpPheProGlyGlyAlaPheLysThrGlySerAl 160 CCTCCAGAACTCAGAGTGGCTGCTCTTAGATCAACACATGCTCAAGGTGCATTACCCGAA GCATCGCCCTGGGATAACTTGCGAGAAGCCACCTCCTACCCTAATTTGTAAGACCAGGTG 416 200 596 356 656 476 유 원 밁 δ 밁 S 밁 ð 밁 ð 문 S 문 δ 문 S 밁 S 1317 440 420

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30-JAN-2001;
06-FEB-2001;
19-MAR-2001;
04-APR-2001;
      The invention relates to an isolated polypeptide with signal sequences which allow it to be secreted extracellularly or membrane associated. activity of polypeptides of the invention may be described as, cytostatic, vulnerary, antiarteriosclerotic, antiparkingonian, nootrog
                                                                                                                                                                                                                                                                                                                                                                                                                                    Agarwal P,
Martensen
                                                                                                                                                                                                             Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder
neuroprotective,
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DB; ABP61005.
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A, Rizvi S
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; 2000US-0257048P.

; 2001US-026048P.

; 2001US-026492P.

; 2001US-026797P.

; 2001US-0276988P.

; 2001US-0281535P.

; 2001US-0289622P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORP
                                                                                                                                                            English.
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rum JC, Xie
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and metabolic. Polypeptides and polymucleotides of the invention are conserved to asset in the treatment, or as a vaccine in the prevention of, cancer, common healing disorders, infection, atherosclerosis, Parkinson's disease confidence of the prevention of, cancer, common healing disorders, autoimmune disorder, haematopoietic disorder, cardiovascular disorders, pancreatitis, respiratory disorders and common diseases, parcoliferation, systemic autoimmune diseases, hyper-immunity, common disorders, pancreatitis, respiratory disorders and covelopmental abnormality, gastrointestinal ulceration, neuropathy, common disorders e.g. hypothyroidism, brain damages, solitis, come photococcurrence e.g. hypothyroidism, brain damages, colitis, come photococcurrence e.g. hypothyroidism, brain damages, solitis, come photococcurrence of the monomalities, and alleviation of precocious puberty. The confidence of the invention in records ABQ86130-ABQ86184 represent novel human cDNA's
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                                              the invention
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Sequence 1746 BP; 401 ð, 464 Ç 459 ი 422 Η, 0 U; 0 Other;

Percent Similarity:
Best Local Similarity:
Query Match:
DB:

2.17e-237 2607.50 92.67% 91.39% 84.69%

Length:
Matches:
Conservative:
Mismatches:
Indels:

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S 밁 Ş 밁 Ś 밁 ð 망 δ 밁 Ś 밁 ð 밁 S 밁 Ś 밁 Ś 밁 S US-10-023-515-2 (1-581) x ABQ86170 (1-1746) 212 556 192 496 172 436 152 376 316 132 112 256 196 136 92 72 52 76 32 40 12 TrpCysPhePheLeuIleLeuGlnProLeuLeuGlyHisArgGlnTrpGlyLysThrGly GTCCAGAAGAACATCGAGTTCTTCGGTGGGG ValGlnLysAsnIleGluPheDheGlyGlyAspProSerSerValThrIlePheGlyGlu TrpAspGlnHisAlaFroGlyAsnTrpAlaPheLysAspGlnValAlaAlaLeuSerTrp GAGGACGTGCTGGTTGTGGTCCTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACCACA GluAspValLeuValValValValGlnTyrArgLeuGlyIlePheGlyPhePheThrThr GlyGlyAlaPheLy8ThrGlySerAlaSerIlePheAspGlySerAlaLeuAlaAlaTyr HisMetLeuLysValHisTyrDroLysPheGlyValSerGluAspCysLeuTyrLeuAsn 131 researcascarscreeseaacressecrircaassaccassrescrecrererecres GGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCCTAT ATCTATGCGCCTGCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTCCCA CATATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTGAAC 375 GluAlaThrSerTyrProAsnLeuCysLeuGlnAsnSerGluTrpLeuLeuLeuAspGln 111 GAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGATCAA 315 ccerrecearceceárriaceaacececaecerecarcecerecearaacriecea ProLeuGlySerLeuArgPheThrAsnProGlnProAlaSerProTrpAspAsnLeuArg ACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCTTTGCTGCTCCC ProSerAlaGluGlyProGlnArgAsnThrArgLeuGlyTrpIleGlnGlyLysGlnVal TGGGCTATCTGGGTCCTTGCAGCCCCCC-------ACCAAAGGG ThrValLeuGlySerProValProValAsnValPheLeuGlyValProPheAlaAlaPro 231 615 211 555 191 171 435 495 255 91 195 71 135 51 31 75

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Yamamoto
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24-JAN-2002;
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Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease; gene; ss.
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2002US-0350435P.
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Otsuki T, Wakamatsu A, Sato H,
Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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                             Ishii S;
R, Tamechika I;
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New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy. 'n

SEQ ID NO 736; 205pp; English.

The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.

428 A; 541 C; 473 G; 520 T; U; 0 Other;

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                                   Length:
Matches:
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Indels:
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GluAlaThrSerTyrProAsnLeuCysLeuGlnAsnSerGluTrpLeuLeuLeuLspGln
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29-MAY-2001;
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LeuGlnProPhePhePhePheCysAlaPro
 standard;
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                                                                                                                                                                                                                                                    CTGTCTCTGTGGCCAGCTTATAATCTGACTGAGCAGTACCTCCAGCTGGACTTGAACATG
                                                                                                                                                                                                                                                                           LeuSerLeuTrpProAlaTyrAsnLeuThrGluGlnTyrLeuGlnLeuAspLeuAsnMet
                                                                                                                                                                                                                                                                                                                                        ArgLysMetMetLysTyrTrpAlaThrPheAlaArgThrGlyAsnProAsnGlyAsnAsp
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(first

polynucleotide #98.

Human; NOVX; gene; ss; metabolic disorder; cardiomyopathy; diabetes; ASD; hypertension; congenital heart defect; aortic stenosis; valve disease; atrial septal defect; atrioventricular canal defect; ductus arteriosus; pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD, tuberous sclerosis; scleroderma; atherosclerosis; infectious disease; obesity; anorexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; haemophilia; hypercoagulation; Crohn's disease; cancer.

WO200281498-A2

2002WO-US010780

7 2001US-0281086P.
7 2001US-0281136P.
7 2001US-0281863P.
7 2001US-0281906P.
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7 2001US-0282934P.
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7 2001US-0285381P.
7 2001US-0285381P.
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7 2001US-0285606P.
7 2001US-028606P.
7 2001US-028629P.
7 2001US-0287213P.
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14-NOV-2001
21-NOV-2001
04-DEC-2001
04-DEC-2001
03-JAN-2002
16-JAN-2002
16-JAN-2002
                                                                                                                                                                                                                                                           The invention relates to human polypeptides, termed NOVX, and the polymucleotides encoding them. The polypeptides and polymucleotides are useful for diagnosing disease, and screening for potential therapeutic agents. The sequences are useful for treating metabolic disorders, cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD), atrioventricular canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative disorders, hatpainer's disease, Parkinson's disease, immune disorders, haematopoletic disorders, haemophilia, hypercoagulation, Crohn's disease and cancer. Sequences ABX72170-ABX72275 represent human NOVX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guo X, Kekuda R, Miller CB, Malyankar UM, Spytek KA;
Patturajan M, Liu X, Gusev VY, Li L, Vernet CAM, Zerhusen BD;
Gorman L, Shenoy SG, Pena CBA, Smithson G, Burgess CB, Gerlach
Padigaru M, Shimkets RA, Gangolli EA, Taupier RJ, Casman SJ, Ji
Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ;
Macdougall JR, Rothenberg MB, Mazur A, Millet I, Peyman JA;
Ellerman K;
                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated NOVX polypeptide useful for treating atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease and cancer.
                                                                                                                                                                                                                                          Sequence
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P-PSDB; ABU54639.
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                                                                                                                                                                                                                              AspLeuLeuSerGlnLysAlaPheLysAlaIleProSerIleIleGlyValAsnAsnHis 350
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                      IleThrAlaArgTyrHisArgAspAlaGlyAlaProValTyrPheTyrGluPheArgHis 443
                                                               GluIleArgAspSerLeuLeuAspLeuLeuGl
                                                                                               CCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAGCACTCCCTGACT
                                                                                                           ProProGlnTyrLeuHisLeuValAlaAsnGluTyrPheHisAspLysHisSerLeuThr
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20-OCT-2000; 2000US-024233P.
09-NOV-2000; 2000US-024951P.
16-NOV-2000; 2000US-0249519P.
22-NOV-2000; 2000US-0252834P.
30-NOV-2000; 2000US-0250567P.
                                   Azimzai Y
Elliott V
Lal P, L
Ring HZ,
Walsh RT,
        WPI; 2002-362498/39.
P-PSDB; ADR19663.
                                                                                                                                                                                                                                                                                                                       drug metabolising enzyme; DME; cytostatic; immunosuppressive; antiinflammatory; endocrine; ophthalmological; gastrointestinal; hepatotropic; cancer; cell prollferative disorder; autoimmune disorder; inflammatory disorder; endocrine disorder; eye disorder; gastrointestinal disorder; liver disorder; metabolic disorder; gene; ds
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                                 i Y, Baughin MR, B
t VS, Gandhi AR, G
Lee EA, Lu DAM, I
IZ, Sanjanwala MS, Y
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/product= "Human
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1. .1857
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                             Borowsky ML, Ding L, Duggan BM;
Griffin JA, Hafalia AJA, Ison CH, K!
Mguyen DB, Arvizu C, Policky JL, R:
Tang YT, Tribouley CM, Narinder WK;
U Y, Yang J, Yao MG, Yue H;
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Human drug metabolizing enzymes, useful disorders associated with aberrant (DME) autoimmune disorders. in the diagnosis activity, e.g., and treatment cancer and 0£

Claim 12; SEQ ID NO 20; 142pp; English

This invention relates to novel drug metabolising enzymes (DME) and the nucleotide sequences which encode them. The invention may be useful for the development of compounds with a cytostatic, immunosuppressive, antiinflammatory, endocrine, ophthalmological, gastrointestinal or hepatotropic activity acting as an agonist or antagonist of drug metabolising enzyme activity. The invention may be used in the diagnosis and treatment of disorders associated with decreased or increased expression or activity of drug metabolising enzymes. Such disorders expression or activity of drug metabolising enzymes. Such disorders include cancer, cell proliferative disorders, autoimmune/inflammatory, metabolic disorders. The present sequence is that of a gene which encodes a human drug metabolising enzyme (DME) of the invention. Note: This sequence did not form part of the printed specification but was obtained in electronic format from EPO.

Sequence 1857 B₽; 428 A; 487 Ç 496 ູດ 446 H, 0 U; 0 Other;

No.:

δ 닭 δ 밁 δ 밁 δ Ş 밁 S 밁 맑 δ 밁 S 문 S 밁 Ş Percent Similarity:
Best Local Similarity:
Query Match:
DB: Score: US-10-023-515-2 (1-581) x ADR19681 (1-1857) 211 754 191 694 171 634 574 151 131 514 111 454 394 334 274 91 71 51 31 TGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGC TrpValGlnLysAsnIleGluPhePheGlyGlyAspProSerSarValThrIlePheGly TATGAGGACGTGCTGGTTGTGGTCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACC TyrGluAspValLeuValValValValGlnTyrArgLeuGlyIlePheGlyPhepheThr ProGlyGlyAlaPheLysThrGlySerAlaSerIlePheAspGlySerAlaLeuAlaAla AsnIleTyrAlaProAlaHisAlaAspThrGlySerLysLeuProValLeuValTrpPhe GlnHisMetLeuLysValHisTyrProLysPheGlyValSerGluAspCysLeuTyrLeu 130 ValThrValLeuGlySerProValProValAsnValPheLeuGlyValProPheAlaAla 70 CCAGGAGGTGCCTTCAAGACTGGCT AACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCCGTCTTGGTGGTTC CAACATATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTG CGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGAT 513 ArgGluAlaThrSerTyrProAsnLeuCysLeuGlnAsnSerGluTrpLeuLeuLeuAsp CCCCCCCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG ProProLeuGlySerLeuArgPheThrAsnProGlnProAlaSerProTrpAspAsnLeu 90 ercaererecreseaadecerereceresadecererreceresadrecererriecre 1.52e-235 2588.50 94.62% 94.42% 84.07% PCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCC Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 1857 491 5 5 23 230 813 210 753 190 693 170 150 633 573 453 393 50

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RESULT 11
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                                                                                                       MetSerLeuGlyGlnArgLeuLysGluProArgValAspPheTrpThrSerThr11ePro
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                                                                                                                                                                                                       SerArgLysMetMetLysTyrTrpAlaThrPheAlaArgThrGlyAsnProAsnGlyAsn
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Novel cauxin protein or its salt, useful
                                                                                                                                                                                                                  cat; cauxin; cat kidney disease marker; kidney disease; gene; ss.
                                                                                                                                       WPI; 2004-002277/01.
                                                                                                                                                            04-MAR-2002; 2002JP-00057908
                                                                                                                                                                       04-MAR-2002; 2002JP-00057908
                                                                                                                                                                                  09-SEP-2003
                                                                                                                                                                                             JP2003250575-A.
                                                                                                                                                 (TOHO-) TOHOKU TECHNOARCH KK
                                                                                                                diagnosing cat kidney disease.
                                                                                                                       as
                                                                                                                       a cat
                                                                                                                       kidney
                                                                                                                       disease
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Claim 6; SEQ ID NO 3; 33pp; Japanese.

The present sequence encodes a cat cauxin protein (I) or its salt, which CC is cat kidney disease marker. Also described: (I) a partial peptide (II) cf (I); (2) a nucleic acid (III) encoding (I) or (II); (3) a vector (IV) CC comprising (III); (4) a transformed host (V) comprising (III) or (IV); (5) producing (I) or (II) by culturing (V); (6) a antibody (VI) which CC couples specifically with (I) or (II); (7) diagnosing cat kidney disease CC which involves measuring (I) quantitatively, and where reduction of CC amount of (I) indicates presence of the disease; (8) a cat kidney disease CC diagnostic agent comprising (I) labelling agent, a reagent which measures CC the biological activity of urinary (I) or (VI); and (9) a cauxin CC cat kidney disease marker and (VI) is useful for diagnosing cat kidney CC disease. (I) enables detection of cat kidney disease simply and CC complicated diagnostic methods such as X-ray imaging, ultrasonic imaging, CC complicated diagnostic methods such as X-ray imaging, ultrasonic imaging, blood testing.

Sequence 2145 BP; 444 A; 581 C; 550 G; 564 T; 0 U; 6 Other;

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Best Local Similarity:
Query Match:
DB:
                        Percent Similarity:
                                Score:
                                        Pred. No.:
                                               Alignment Scores:
5.74e-181
2015.00
80.87%
70.04%
65.44%
                       Length:
Matches:
Conservative:
        Mismatches:
Indels:
2145
388
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US-10-023-515-2 (1-581) x ADF50146 (1-2145)

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                                              GlnHisMetLeuLysValHisTyrProLysPheGlyValSerGluAspCysLeuTyrLeu 130
AsnIleTyrAlaProAlaHisAlaAspThrGlySerLysLeuProValLeuValTrpPhe 150
                                                                                  CGAAATGCCACATCCTAACCTAAATTATGCTTCCAGGACTTAGAGTGGCTGGTCTCCTAT 477
                                                                                                  ArgGluAlaThrSerTyrProAsnLeuCysLeuGlnAsnSerGluTrpLeuLeuLeuAsp
                                                                                                                                        CCTCCTAGGGCCCCTGCGATTTAAGCAACCAAAGCCTGCTCTGCCCGGGAATGACTTC
                                                                                                                                                       ProProLeuGlySerLeuArgPheThrAsnProGlnProAlaSerProTrpAspAsnLeu
                            CAACACGTTCTCAAAGTGCGTTACCCCAAATTGGAAGCGTCCGAAGACTGCCTGTACCTT
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Cat cauxin encoding cDNA SEQ ID NO:3.

12-FEB-2004 ADF50146;

(first entry)

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LeuSerArgLysMetMetLysTyrTrpAlaThrPheAlaArgThrGlyAsnProAsnGly
                                                                     GlyAlaPheLeuLysGlyAspIleValMetPheGluGlyAlaThrGluGluGluLysLeu
                                                                                                               GTGCCTTCCTGAAAGGCGACATTGTCATGTTCGAAGGAGCCACCGAGGAGGAGAAATTG
                                                                                                                                AspThrLysProAlaPheValLysAlaAspHisAlaAspGluValArgPheValPheGly 469
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                                                                                                                                                                                                                                                                LeuAspLeuLeuGlyAspValPhePheValValProAlaLeuIleThrAlaArgTyrHis 429
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                                                            The present sequence encodes a cat cauxin protein (I) or its salt, which CC is cat kidney disease marker. Also described: (I) a partial peptide (II) co of (I); (2) a nucleic acid (III) encoding (I) or (II); (3) a vector (IV) (CC comprising (III); (4) a transformed host (V) comprising (III) or (IV); (CC couples specifically with (I) by culturing (V); (6) a antibody (VI) which (CC couples specifically with (I) or (II); (7) diagnosing cat kidney disease (CC which involves measuring (I) quantitatively, and where reduction of (I) indicates presence of the disease; (8) a cat kidney disease (CC diagnostic agent comprising (I) labelling agent, a reagent which measures (CC disease; (I) enables detection of (I) is useful as a cc disease (I) enables detection of cat kidney disease simply and (CC complicated diagnostic methods such as X-ray imaging, ultrasonic imaging, cc block feating the formal rearring.
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19-DEC-2000; 2000US-0256710P
                                    17-DEC-2001; 2001WO-US049232.
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09-JAN-2001;
30-JAN-2001;
06-FEB-2001;
19-MAR-2001;
04-APR-2001;
08-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a polypeptide-human carboxylatase-24.64, the polymucleotide for coding it, the process for preparing the polypeptide by DNA recombination, the application of the polypeptide in treating diseases such as primary hypertension, digestive ulcer, nephrotic, bronchial asthma, tremor, etc, the antagon of the polypeptide and its medical action, and the application of the polymucleotide are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1244
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                                                                                                                           ATCCTGCACATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAG
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                                                                             GAGGCTCCTGAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAAC
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                       New peptides and its encoding nucleic acid derived from intestinal carboxyesterase, useful as immunostimulants for treating cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1680 BP; 345 A; 475 C; 488 G; 372 T; 0 U; 0 Other;
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                MetAlaLysGlyLeuPheHisLysAlaIleMetGluSerGlyValAlaIleIleProTyr 265
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CACAGGCTCCAGTTCTGGAAGAAGGCGCTGCCC
                              ProArgValAspPheTrpThrSerThrIlePro 550
                                                          CAGGAGGAGCAATACCTGCAGCTGAACCTACAGCCTGCGGTGGGCCGGGCTCTGAAGGCC
                                                                             LeuThrGluGlnTyrLeuGlnLeuAspLeuAsnMetSerLeuGlyGlnArgLeuLysGlu
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                                                                                                                                                                                                                                                                       HisAlaAspGluValArgPheValPheGlyGlyAlaPheLeuLysGlyAspIleValMet 479
                                                                                                                                                                                                                                                                                                        GAGTTCCAGCATCAGCCCAGCTGGCTCAAGAACATCAGGCCACCGCACATGAAGGCAGAC
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Maximum DB
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-MODEL-frame+ p2n.model -DEV=xlh
-Q-(gnn2 1/USFTO spool/6664091/runat 14062005 133643 10569/app query.fasta_1.775
-Q-(gnn2 1/USFTO spool/6664091/runat 14062005 133643 10569/app query.fasta_1.775
-DB=Published Applications NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINNATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -STRATT=1 -END=-1 -MARRIX=bits sumc2
-TRANS=human40.cdi -LIST=45 -DCCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -QUTFMT=pto -NORM=ext -HEAPSIZES-500 -MINLEN=0
-MAXIEN=2000000000 -USER=66640P GCGN 1 480 @runat 14062005 133643 10569
-NCPU=6 -ICPU=3 -NO MMAP -LARGRQÜERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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seq length:
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Fgapop 6.0
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Copyright (c) 1993 - 2005 Compugen Ltd.
                 / Cgm2 6/ptodata/1/pubpna/USO9A PUBCOMB.seq:*
/ Cgm2 6/ptodata/1/pubpna/USO9B PUBCOMB.seq:*
/ Cgm2 6/ptodata/1/pubpna/USO9B PUBCOMB.seq:*
/ Cgm2 6/ptodata/1/pubpna/USO9 NEW PUB.seq:*
/ Cgm2 6/ptodata/1/pubpna/USO9 NEW PUB.seq:*
/ Cgm2 6/ptodata/1/pubpna/USOA PUBCOMB.seq:*
/ Cgm2 6/ptodata/1/pubpna/USOA PUBCOMB.seq:*
/ Cgm2 6/ptodata/1/pubpna/USOD PUBCOMB.seq:*
/ Cgm2 6/ptodata/1/pubpna/USOD PUBCOMB.seq:*
/ Cgm2 6/ptodata/1/pubpna/USOP PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/PCT_N
/cgn2_6/ptodata/1/pubpna/US06_
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6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1 US-10-023- Sequence Publicat: GENERAL APPLICAL APPLICAL FILE OI FILE RE CURRENT CURRENT CURRENT CURRENT PRIOR FI PRIOR AI PRIOR FI		44444333333333333333333333333333333333	Result
515-3 3, Application 3, Application ion No. US20020: INFORMATION: NT: CUrtis, ROIVITIS, SANC: FINVENTION: 53 FINVENTION: 53 FINVENTION: DATE: APPLICATION NUMBIFILING DATE: 2001 PPLICATION NUMBIFILING DATE: 2001		3079 3079 3079 3079 3079 3079 3079 3079	201
		I	Query
		1746 2158 2158 2158 2158 2158 2158 2158 2158	
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0023515 3A1 7. Inmaculada INMACULADA CARBOXYLESTERASE NOVEL HUMAN CARBOXYLESTERASE NEMBER AND USES THEREOF US/10/023,515 US/10/023,515 1/2-18 1/2-18 1/2-18	ALIGNMENTS	US-10-023-515-3 US-10-674-636-3 US-10-674-636-1 US-10-674-636-1 US-10-674-636-1 US-10-674-636-1 US-10-10-451-168-40 US-10-10-451-168-41 US-10-10-233-933A-3 US-10-10-233-933A-3 US-10-233-933A-3 US-10-233-933A-3 US-10-233-933A-3 US-10-233-933A-3 US-10-233-933A-3 US-10-233-933A-3 US-10-233-933A-3 US-10-233-933A-3 US-10-233-933A-3 US-10-233-934-1 US-10-287-367C-829 US-10-843-641A-829 US-10-843-641A-829 US-10-843-641A-829 US-10-843-641A-829 US-10-843-641A-829 US-10-843-641A-829 US-10-10-843-641A-829 US-10-10-83-641A-829 US-10-10-10-83-641A-829 US-10-10-10-83-641A-829 US-10-10-10-83-641A-831 US-10-10-10-10-10-10-10-10-10-10-10-10-10-	1
ASE		Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 40, Appl Sequence 23, Appl Sequence 23, Appl Sequence 135, Appl Sequence 195, Appl Sequence 195, Appl Sequence 195, Appl Sequence 1, Appli Sequence 1038, Appli Sequence 1038, Appli Sequence 1038, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 271, Appli Sequence 271, Appli Sequence 410, Appli Sequence 410, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 22, Appli Sequence 541, App Sequence 541, App	Description

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; LENGTH: 1746
; TYPE: DNA
; ORGANISM: Homo :
US-10-023-515-3
                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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SOFTWARE: FASTSEQ for Windows
SEQ ID NO 3
LENGTH: 1746
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Matches:
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Mismatches:
Indels:
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RESULT 2
US-10-674-636-3
Sequence 3, Application US/10674636
; Publication No. US20040086922A1
; GENERAL IMFORMATION:
; APPLICANT: CUITIS, ROTY A. J.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: 53010, A NOVEL HUMAN
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  CARBOXYLESTERASE
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CURRENT APPLICATION NUMBER: US/10/674,636
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: US/10/023,515
PRIOR FILING DATE: 2001-12-18
PRIOR PILING DATE: 2001-12-18
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1746
TYPES: DNA
ORGANISM: Homo Sapiens
US-10-674-636-3
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                                        AlaPheLysAspGlnValAlaAlaLeuSerTrpValGlnLysAsnIleGluPhePheGly
                                                                                                                                                  SerIlePheAspGlySerAlaLeuAlaAlaTyrGluAspValLeuValValValValGln
                                                                                                                                                                                                       GlySerLysLeuProValLeuValTrpPheProGlyGlyAlaPheLysThrGlySerAla
                                                                                                                                                                                                                                          TTCGGAGTGTCAGAAGACTGCCTCTACCTGAACATCTATGCGCCCTGCCCACGCCGATACA
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Sequence 1, Application US/10023515
Publication No. US20020182636A1
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A. J.
APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-122001
CURRENT APPLICATION NUMBER: 60/256,369
PRIOR APPLICATION NUMBER: 60/256,369
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/279,508
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FRASESEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2158
TYPE: DNA
ORGANISM: Homo sapiens
PAME/KEY: CDS
LOCATION: (96)...(1838)
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                                                                             PheAlaArgThrGlyAsnProAsnGlyAsnAspLeuSerLeuTrpProAlaTyrAsnLeu
                                                                                                                              GAAGGAGCCACGGAGGAGGAGAAGTTACTGAGCCGGAAGATGATGAAATACTGGGCTACC 1595
                                                                                                                                                  GluGlyAlaThrGluGluGluLysLeuLeuSerArgLysMetMetLysTyrTrpAlaThr
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| Sequence 45, Application US/10757262 | Fublication No. US200401978281 | GREBRAL INFORMATION: | RepLICANT: Karlchedt; Venkateswarlu | APPLICANT: Karlchedt; Venkateswarlu | APPLICANT: Karlchedt; Venkateswarlu | APPLICANT: Eliaso-Santiago, Inmaculada | APPLICANT: Eliaso-Santiago, Inm
                           LENGTH: 2158
TYPE: DNA
ORGANISM: Homo E
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RESULT 6
US-10-451-168-40
US-10-451-168-40
Sequence 40, Application US/10451168
Publication No. US20040091969A1
GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: GLIAXO GROUP LIMITED
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50039
CURRENT APPLICATION NUMBER: US/10/451,168
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PRIOR APPLICATION NUMBER: PCT/USO1/49232
PRIOR FILING DATE: 2000-12-17
PRIOR FILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR APPLICATION NUMBER: 60/289,622
PRIOR PILING DATE: 2001-04-04
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292 GluAlaLeuLeuArgCysLeuArgThrLysProSerLysGluLeuLeuThrLeuSerGln
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            IleLeuSerAlaSerAspMetLeuHisSerProLeuSerSerLeuThrPheLeuSerLeu
                                                                                                                                                              LeuSerLeuTrpProAlaTyrAsnLeuThrGluGlnTyrLeuGlnLeuAspLeuAsnMet 531
                                                                                                                                                                                                                 SerLeuGlyGlnArgLeuLysGluProArgValAspPheTrpThrSerThr1leProLeu 551
                                                                                                                                  CTGTCTCTGTGGCCAGCTTATAATCTGACTGAGCAGTACCTCCAGCTGGACTTGAACATG 1575
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                                                                                                                                                                                                                                                                                                TTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGAGGAAGTTACTGAGC 1455
                                                                                                                                                                                                                                                                                                                        PheLeuLysGlyAspIleValMetPheGluGlyAlaThrGluGluGluLysLeuLeuSer
                                                                                                                                                                                                                                                                                                                                                                                AAGCCAGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTTCGGTGGTGCC
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SAUVANWALA, Madhusudan M.; YAO, Monique G.
APPLICANT: AU-YOUNG, Janice K.; BAUGHN, Mariah R.
APPLICANT: ARVIZU, Chandra S.; RING, Huijun Z.
APPLICANT: LEE, Ernestine A.; DING, Li
APPLICANT: LEE, Ernestine A.; DING, Li
APPLICANT: VIE, Henry; TRIBOULEY, Catherine M.
APPLICANT: UL, DYUNG AINE M.; LAL, Preeti G.
APPLICANT: UL, DYUNG AINE M.; LAL, Preeti G.
APPLICANT: WARREN, Bridget A.; YANG, Jumming
APPLICANT: GHAWLA, Natinder K.; NGUYEN, Danniel B.
APPLICANT: ISON, Craig H.
TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
FILL REFERENCE: PI-0313 USN
CURRENT APPLICATION NUMBER: US/10/433,256
CURRENT FILING DATE: 2003-05-30
FRIOR APPLICATION NUMBER: US/10/433,256
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: US 60/254,308
PRIOR APPLICATION NUMBER: US 60/254,308
PRIOR APPLICATION NUMBER: US 60/256,189
PRIOR APPLICATION NUMBER: US 60/257,713
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 60/257,713
PRIOR FILING DATE: 2001-01-9
PRIOR APPLICATION NUMBER: US 60/266,020
PRIOR FILING DATE: 2001-01-9
PRIOR APPLICATION NUMBER: US 60/266,020
PRIOR FILING DATE: 2001-01-9
PRIOR APPLICATION NUMBER: US 60/266,020
PRIOR FILING DATE: 2001-02-02

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SOFTMARE: BERL PROGRAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 6538080CB1
US-10-433-256-23
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US-10-433-256-23
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LENGTH: 2232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                334
                                                                                                                                                                                                                 274
91 ArgGluAlaThrSerTyrProAsnLeuCysLeuGlnAsnSerGluTrpLeuLeuLeuAsp 110
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                                                                                                                       GTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCCTTTGCTGCT
                                                                ProProLeuGlySerLeuArgPheThrAsnProGlnProAlaSerProTrpAspAsnLeu
                                                                                                                                             ValThrValLeuGlySerProValProValAsnValPheLeuGlyValProPheAlaAla
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	1474 GATGCTGGTGCACCTGTCTATGAGTTTCGGCACCGGCCTCAGTGCTTTGAAGAC 1533 451 ThrLysProAlaPheValLysAlaAspHisAlaAspGluValArgPheValPheGlyGly 470 	성 음
Db 237 CTCGGAGTCCCCTTTGCTGCTCCCC Qy 84 AlaSerProTrpAspAsnLeuArgG	AspAlaGlyAlaProValTyrPheTyrGluPheArgHisArgProGlnCysPheGluAsp	8 8
Qy 64 LeuGlyValProPheAlaAlaProProLeuGlySerLeuArgPheThrAsnProGlnPro	euGlyAspValPhePheValValProAlaLeuIleThrA 	§ 8
44 0	391 ValalaAsnGluTyrPheHisAspLysHisSerLeuThrGluIleArgAspSerLeuLeu 410 	유 성
6	371 SerLeuAlaLeuHisLeuIleGlnAsnIleLeuHisIleProProGlnTyrLeuHisLeu 390 	용 <i>성</i>
ry Match: 93.44% 17 10-003-515-2 (1.581) v HS-10-104-04	351 GluCysGlyPheLeuLeuProMetLysGluAlaDroGluIleLeuSerGlySerAsnLys 370 	B 8
Pred. No.: O Length: Pred. No.: Score: Score: Percent Similarity: P	331 AspleuleuSerGlnlysalaPheLysalaIleProSerIleIleGlyValAsnAsnHis 350 	B 8
1 H	311 GlnLysThrLysSerPheThrArgValValAspGlyAlaPhePheProAsnGluProLeu 330 	B 8
; SOFTWARE: PATENTIN Ver. 2.1 ; SEQ ID NO 249 ; LENGTH: 2092	291 SerGluAlaLeuLeuArgCysLeuArgThrLysProSerLysGluLeuLeuThrLeuSer 310	B 8
CURRENT FILING DATE: 2002-03-25 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: NUMBER OF SEO ID NOS: 4096	271 TyrGluLysSerGluAspLeuGlnValValAlaHisPheCysGlyAsnAsnAlaSerAsp 290 	음 성
APPLICANT: HELIX RESEARCH INSTITUTE ; APPLICANT: HELIX RESEARCH INSTITUTE ; TITLE OF INVENTION: NO. US20030236392A1e1 ; FILE REFERENCE: H1-A0105 ; CURRWAT APPLICATION NUMBER. US/10/104 047	251 PheHisLysAlaIleMetGluSerGlyValAlaIleIleDroTyrLeuGluAlaHigAsp 270	B 8
US-10-104-047-249 US-10-104-047-249 ; Sequence 249, Application US/10104047 ; Publication No. US20030236392A1	231 GluSerAlaGlyAlaIleSerValSerSerLeuIleLeuSerProMetAlaLy8GlyLeu 250 	B 8
	211 TrpValGlnLygAsnIleGluPhePheGlyGlyAspProSerSerValThrIlePheGly 230	B 8
	191 ThrTrpAspGlnHisAlaProGlyAsnTrpAlaPheLysAspGlnValAlaAlaLeuSer 210 	용 성
1774	171 TyrGluAspValLeuValValValValGlnTyrArgLeuGlyIlePheGlyPhePheThr 190 	음 성
1714	151 ProGlyGlyAlaPheLysThrGlySerAlaSerIlePheAspGlySerAlaLeuAlaAla 170 	B 8
The spice of the state of the s	131 AsnīleTyrAlaProAlaHisAlaAspThrGlySerLysLeuProValLeuValTrpPhe 150 	B 8
1594	111 GlnHisMetLeuLysValHisTyrProLysPheGlyValSerGluAspCysLeuTyrLeu 130 	8 8
Db 1534 ACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTTCGGTGGT		뭥

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460 sAlaAspGluValArgPheValPheGlyGlyAlaPheLeuLysGlyAspIleValMetPh
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                                                                               Percent Similarity:
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DB:
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APPLICANT: SMITHKLINE BEECHAM p.1.c.
APPLICANT: SMITHKLINE BEECHAM p.1.c.
APPLICANT: SMITHKLINE BEECHAM p.1.c.
APPLICANT: SMITHKLINE BEECHAM p.1.c.
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION. NOVEL COMPOUNDS
FILE REFERENCE: GP50039
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: DCT/US01/49232
PRIOR PILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR APPLICATION NUMBER: 60/289,622
PRIOR FILING DATE: 2001-03-19
PRIOR PILING DATE: 2001-03-19
PRIOR FILING DATE: 2001-04-08
PRIOR FILING DATE: 2001-05-19
PRIOR FILING DATE: 2001-06-28
NUMBER: 60/289,622
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ORGANISM: Homo
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CACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCTGAGGGCCCATGATTAT 795 272 GluLysSerGluAspLeuglnvalValalaHispheCysGlyAsnAsnAlaSerAspSer 291	TrpAspGlnHisAlaProGlyAsnTrpAlaPheLysAspGlnValAlaAlaLeuSerTrp	112 HisMetLeuLysValHisTyrProLysPheGlyValSerGluAspCysLeuTyrLeuAsn 131	12 TrpCysPhePheLeuIleLeuGlnProLeuLeuGlyHisArgGlnTrpGlyLysThrGly
APPLICANT: ISHI, SHIZUKO APPLICANT: ISHNI, SHIZUKO APPLICANT: ISONO, YUUKO APPLICANT: HIO, YURI APPLICANT: HIO, YURI APPLICANT: OTSUKA, KAORU APPLICANT: OTSUKA, KAORU APPLICANT: IRLE, RYOTARO APPLICANT: TAMECHIKA, ICHIRO APPLICANT: OTSUKA, MOTOYUKI APPLICANT: OTSUKA, MOTOYUKI APPLICANT: MAGAHARI, KENUI APPLICANT: MAGAHARI, KENUI APPLICANT: MAGHIKO TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA FILE REFERENCE: 084335/0160 CURRENT APPLICATION NUMBER: US/10/094,749 CURRENT FILING DATE: 2002-03-12 PRIOR APPLICATION NUMBER: 60/350,435 PRIOR APPLICATION NUMBER: 50/350,435 PRIOR FILING DATE: 2001-09-14 NUMBER OF SEQ ID NOS: 3381 SOFTWARE: Patentin Ver: 2.1	5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1	Oy 465 ArgPheValPheGlyGlyAlaPheLeuLysGlyAspIleValMetPheGluGlyAlaThr 484 1396 CGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACG 1455 Qy 485 GluGluGluLysLeuLeuSerArgLysMetMetLysTyrTrpAlaThrPheAlaArgThr 504	LysSerLeuAlaLeu

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; ORGANISM: Homo sapiens
US-10-094-749-736
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                                GluLy8SerGluAspLeuGlnValValAlaHisPheCy8GlyAsnAsnAlaSerAspSer
                                                                                                                                     HisLysAlaIleMetGluSerGlyValAlaIleIleProTyrLeuGluAlaHisAspTyr
                                                                                                  TCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTATTC
                                                                                                             SerAlaGlyAlaIleSerValSerSerLeuIleLeuSerProMetAlaLysGlyLeuPhe
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Sequence 195, Application US/10114270
Publication No. US20040030110A1
GENERAL INFORMATION:
APPLICANT: Guo, Xiaojia
APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles E.
APPLICANT: Miller, Uriel M.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Patturajan, Meera
APPLICANT: Patturajan, Meera
APPLICANT: Liu, Ziaohong
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PRIOR APPLICATION NUMBER: 60/283,710
PRIOR PILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR PILING DATE: 2001-04-17
Remaining Prior Application data removed - See NUMBER OF SEQ ID NOS: 470
SEQ ID NO 195
LENGTH: 1746
TYPE: DNA
ORGANISM: Homo sapiens
PEATURE:
NAME/KBY: CDS
LOCATION: (1)...(1744)
US-10-114-270-195
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APPLICANT: Ji, Weizhen
APPLICANT: Liete, Mario W.
APPLICANT: Liete, Mario W.
APPLICANT: Rastelli, Luca
APPLICANT: Edinger, Shlomit R.
APPLICANT: Stone, David J.
APPLICANT: Stone, David J.
APPLICANT: MacDougall, John R.
APPLICANT: MacDougall, John R.
APPLICANT: MacDougall, John R.
APPLICANT: MacDougall, John R.
APPLICANT: Rothenberg, Mark E.
CURRENT APPLICATION NUMBER: US/10/114,270
CURRENT PILLING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/281,086
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR APPLICATION NUMBER: 60/281,906
PRIOR APPLICATION NUMBER: 60/281,906
PRIOR APPLICATION NUMBER: 60/282,020
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PRIOR APPLICATION NUMBER: 60/283,512
PRIOR APPLICATION NUMBER: 60/283,512
PRIOR APPLICATION NUMBER: 60/283,710
PRIOR PILING DATE: 2001-04-12
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,234
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Shimkete, Richard A.
Gangolli, Esha A.
Taupier Jr., Raymond J.
Casman, Stacie J.
Ji, Weizhen
Pena, Carol B.A.
Smithson, Glennda
Burgess, Catherine B.
Gerlach, Valerie
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Shenoy, Suresh G.
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APPLICANT: MAINGAI, FALIGA DAVINE, FRILIGANT, APPLICANT: BOROWSKY, MARK L., DING, Li;
APPLICANT: BOROWSKY, MARK L., DING, Li;
APPLICANT: GANDHI, Ameena R., GRIFFIN, Jennifer A.;
APPLICANT: KHAN, Brendan; ELLIOTT, Vicki S.;
APPLICANT: KHAN, FARTAH A., LAL, Preeti G.;
APPLICANT: KHAN, FARTAH A., LAL, Preeti G.;
APPLICANT: RAWLUMAR, JENEATH RING, Huijun Z.;
APPLICANT: RAWLUMAR, Jayalaxmi; RING, Huijun Z.;
APPLICANT: RAWLUMAR, Jayalaxmi; RING, Huijun Z.;
APPLICANT: TANG, Y. Tom; TRIBOULEY, Catherine M.;
APPLICANT: TANG, Y. TOM; TRIBOULEY, Catherine M.;
APPLICANT: VANG, JUMMING, MAISH, RODERICK T.;
APPLICANT: VANG, JUMMING; YAO, MONIQUE; YUE, Henry
ITILE OF INVENTION: DRUG METABOLIZING ENZYMES
CURRENT APPLICATION NUMBER: US/10/381,898
CURRENT APPLICATION NUMBER: US/10/381,898
CURRENT APPLICATION NUMBER: US/0/236,947
PRIOR APPLICATION NUMBER: US 60/236,947
PRIOR APPLICATION NUMBER: US 60/236,947
PRIOR APPLICATION NUMBER: US 60/242,323
PRIOR APPLICATION NUMBER: US 60/242,323
PRIOR APPLICATION NUMBER: US 60/247,581
PRIOR APPLICATION NUMBER: US 60/247,581
PRIOR APPLICATION NUMBER: US 60/249,519
PRIOR APPLICATION NUMBER: US 60/249,519
PRIOR APPLICATION NUMBER: US 60/252,834
PRIOR PILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/252,834
PRIOR PILING DATE: 2000-11-16
PRIOR PILING DATE: 2000-11-16
PRIOR PILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/252,834
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20, Application US/10381898

Publication No. US20040086887A1

GENERAL INFORMATION:

APPLICANT: AZIMZAI, Yalda, BAUGHN, Mariah R.;

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APPLICANT: BOROWSKY, Mark L.; DING, Li;

APPLICANT: DUGGAN, Brendan; ELLIOTT, Yicki S.;

APPLICANT: HAFALIA, April J.A.; ISON, Craig H.;

APPLICANT: HAFALIA, April J.A.; ISON, Craig H.;

APPLICANT: KHAN, Farrah A.; LAL, Preeti G.;

APPLICANT: KHAN, Farrah A.; LI, Dyung Aina M.

APPLICANT: ARVIZU, Chandra S.; POLICKY, Jennife:

APPLICANT: RAWKUMARA, Jayalaxmi, RING, Huijun Z.;

APPLICANT: TANG, Y. Tom; TRIBOULEY, Catherine M.

APPLICANT: CHANGLA, Marinder K.; WALSH, Roderick

ADDITCANT: CHANGLA, Narinder K.; WALSH, Roderick
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US-10-381-898-20
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                                                NUMBER OF SEQ ID NOS: 36
SOFTWARE: PERL Program
SEQ ID NO 20
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LENGTH: 1857
TYPE: DNA
ORGANISM: Homo sapiens
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID
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                                                                                                SerGluAlaLeuLeuArgCysLeuArgThrLysProSerLysGluLeuLeuThrLeuSer 310
                                                                                                                                                                                                                                                                  TCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAACCCTCCAAGGAGCTGCTGATCCCTCAGC 1113
                                                                                                                                                     TTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGAGGCCCATGAT
                                                                                                                                                                       PheHisLysalaIleMetGluSerGlyValalaIleIleProTyrLeuGluAlaHisAsp
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Matches:
Conservative:
Mismatches:
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453 90 393 70 333

513

873 230 210

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693

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APPLICANT: Yamashita, Tetsuro
APPLICANT: Miyazaki Masao
TITLE OF INVENTION: CAT KIDNEY DISEASE MARKER
FILE REFERENCE: SHIG PP02US006
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: US/10/233,933A
CURRENT FILING DATE: 2002-09-057908
PRIOR APPLICATION NUMBER: JP2002-057908
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 2145
TYPE: DNA
ORGANISM: Felis Catus
PEATURE:
NAME/KEY: CDS
LOCATION: (175)...(1803)
; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1804)..(2145)

; OTHER INFORMATION: n is :

US-10-233-933A-3
                                                                                                                                                                                                                                                                                                               RESULT 13
US-10-233-933A-3
                                                                                                                                                                                                                                                                         Sequence 3, Application US/10233933A Publication No. US20040214171A1 GENERAL INFORMATION:
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                                   PheHisLysAlaIleMetGluSerGlyValAlaIleIleProTyrLeu---GluAlaHis
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TAGGAGGACGTGCTGATCGTGACTACCCAGTACCGGCTAGGAATATTTGGTTTTTTTCGAC
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Matches:
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Sequence 1, Application US/10233933A

Publication No. US20040214171A1

GENERAL INFORMATION:
APPLICANT: Yamashita, Tetsuro
APPLICANT: Miyazaki, Masao
TITLE OF INVENTION: CAT KIDNEY DISEASE MARKER
FILE REFERENCE: SHIG FP02US006

CURRENT PFLICATION NUMBER: US/10/233,933A

CURRENT FPLICATION NUMBER: US/10/233,933A

CURRENT FILING DATE: 2002-09-03

PRIOR APPLICATION NUMBER: JP2002-057908

PRIOR FILING DATE: 2002-04-03

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 1629

TYPE: DNA

ORGANISM: Felis Catus
                  Alignment Scores:
Pred. No.:
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                            GTAGCCCTATTGACTCAAAAAGCATTTAATTCAGTTCCTTCTATCATCGGAGTCAATAAC
                                          LeuAspLeuLeuSerGlnLysAlaPheLysAlaIleProSerIleIleGlyValAsnAsn
                                                                                     SerGlnLysThrLysSerPheThrArgValValAspGlyAlaPhePheProAsnGluPro 329
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ARPLICANT: SPILINGULAND COMPOUNDS
FILE OF INVENTION: NOVEL COMPOUNDS
FULL REFERENCE: GP50039
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT PILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/US01/49232
PRIOR FILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2000-12-20
PRIOR PILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR FILING DATE: 2001-01-03
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR PILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR PILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR PILING DATE: 2001-03-06
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR APPLICATION NUMBER: 60/266,797
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PRIOR APPLICATION NUMBER: 60/266,797
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PRIOR PILING DATE
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; Sequence 42, Application US/10451168

; Publication No. US20040091969A1

; GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
DB:
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; ORGANISM: Homo sapiens
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                                                                          AlaArgThrGlyAsnProAsnGlyAsnAspLeuSerLeuTrpProAlaTyrAsnLeuThr
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Search Job ti	뭣	ş	Дb	ş
Search completed: June 15, 2005, 15:44:59 Job time : 994 Becs	1009 CCTCTTTCCTTAACTTTCCTCTCTCTCCTCCAGCCTTTCTTT	562 ProLeuSerSerLeuThrPheLeuSerLeuLeuGlnProPhePhePhePheCygAlaPro 581	949 GTGGATTTTTGGACCAGCACCATCCCCCTGATCCTGTCTGCCTCCGACATGCTCCACACATGCTCCACACT 1008	542 ValAspPheTrpThrSerThrIleProLeuIleLeuSerAlaSerAspMetLeuHisSer 561

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 2000000000
                                                                                    A Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2003s:*
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2582.848 Million cell updates/sec
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3079
1 MPQGLTSSASQWCFFLILQP......PLSSLTFLSLLQPFFFFCAP 581
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SUMMARIES

2222211855 54432 222221185 55432	, ₁	Result No.
3079 2900 2607-2900 2607-2606 2597-5 2587-5 2587-5 2454 1985 1985 1780 1230 1230 1230 1230 1230 1230 1230 123	3079	Score
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ADQ89094 ABP61004 ABP61005 ADM84114 ABP61005 ADA54807 ADB19663 ADB19663 ADB750145 ADP50145 ADP50147 ABP61006 AAB20911	ABB79537	ID
Adg89994 Human uro Abp61004 Novel hum Aae25025 Human dru Abm84114 Human dia Abp61005 Novel hum Ada54807 Human pro Adu54639 Human pro Adu54663 Human pro Adf19663 Human pro Adf50145 Cat cauxi Adf64065 Human pro Adf50147 Cat cauxi Adp61006 Novel hum Aae20911 Rat carbo Aab58981 Breast an Adg98219 Human int Aab51981 Breast an Adg98219 Human car Add46521 Human car Add46521 Human pro Aae30960 Human car Add46521 Rat prote Abu53222 Human met Add46521 Rat prote Abu53222 Human met Add46519 Rat prote Add46521 Rat prote	Human	ion

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38.3	38.3	38.3	38.3	38.3	38.3	38.3	38.3	38.3	38.3	38.3	38.3	38.3	38.3	38.3	38.3	38.3	38.3	38.3	38.4
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Abu81549	Abu67116	Abu82152	Abo25111	Abu69085	Abu59921	Abu66840	Abo19424	Abu81140	Abo33809	Abu80843	Abu69108	Abo17886	Abg64341	Abb84949	Aau83696	Aae04101	Aau12442	Aay71107	Abg10273
Human	Human	Novel	Human	Human	Novel	Human	Human	Human	Novel	Human	Human	Novel	Human	Human	Human	Human	Human	Human	Nove1
sec	960	hum	860	PRO	Bec	PRO	Sec	PRO	hum	PRO	PRO	hum	alb	PRO	PRO	gen	PRO	Hyd	hum

ALIGNMENTS

23-SEP-2002 ABB79537; ABB79537 standard; protein; 581 (first entry) Å

Human carboxylesterase family member 53010.

Carboxylesterase; enzyme; human; analgesic; nootropic; antiinflammatory; diagnosis; therapy.

Homo sapiens.

RESULT 1
ABB79537
ID ABB7
XX
AC ABB7
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AC ABB7
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Clark
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Cla Active-site Region Domain Protein Peptide /note= /note= "predicted carboxylesterase type-B signature" 219. .234 44. .545 Location/Qualifiers /note= /label= Mature_protein label= Signal_peptide . 135 . 581 "carboxylesterase domain" "predicted carboxylesterase type-B serine active

WO200250256-A2

27-JUN-2002.

18-DEC-2001; 2001WO-US049075.

18-DEC-2000; 2000US-0256369P. 28-MAR-2001; 2001US-0279508P.

(MILL-) MILLENNIUM PHARM INC.

Curtis RAJ, Silos-Santiago

WPI; 2002-547936/58. N-PSDB; ABN84302.

53010 nucleic acids, useful for diagnosing and treating e.g. vascular diseases, autoimmune diseases, or neurodegenerative diseases; as surrogate markers, in tissue typing and chromosome mapping.

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AC ADQ8
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Matches 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cc protein containing the structural characteristics of a carboxylesterase CC family member. The invention provides 53010 nucleic acids, antisense CC molecules, expression vectors, host cells, transgenic animals, 53010 cc proteins, fusion proteins, antigenic peptides, anti-53010 antibodies and CC methods for detecting the presence of 53010 polypeptides or nucleic acids, of identifying a compound that binds to the 53010 polypeptide, and compound that binds to the 53010 polypeptide, and compound that binds to the 53010 polypeptide, and controlling disorders involving aberrant or deficient hydrolysis of controlling disorders involving aberrant or deficient hydrolysis of carboxylic esters. As 53010 mRNA is highly expressed in the central and peripheral nervous system, and its expression is regulated in some rodent therapeutic agents for controlling neurological disorders, such as pain-related disorders. A claimed method of treating or preventing a disorder of a 53010-expressing cell involves administering a compound that condulates 53010 activity or expression
                               ADQ89094 standard;
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                                                                                                                                                         EGATEEEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNNSLGQRLKSP
                                                                                                                                                                                                                   PALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMF
                                                                                                                                                                                                                                      PALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMF
                                                                                                                                                                                                                                                                               APEILSGSNKSLALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVV
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                               protein;
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                                                                                                                                                                                   Query Match
Best Local (
                                                                                                                                                                                                                            Sequence
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27-MAR-2003;
08-MAY-2003;
19-MAY-2003;
16-JUN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of polypeptides related to urological disorders, e.g. 44390, 54181, 211 or for identifying a compound capable of treating a urological disorder or identifying and treating a subject having a urological
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02-SEP-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  urological disorder; uropathic; cytostatic; urinary incontinence;
benign prostatic hyperplasia; human.
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                                                                                                 1; SEQ ID NO 46;
                                                                                                                                                                                 Similarity
FGVSEDCLYLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQ
                                            NVFLGVPFAAPPLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLLDQHMLKVHYPK
                                                                NVFLGVPFAAPPLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHMLKVHYPK 120
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2003US-0457901P
2003US-0468775P
2003US-0471614P
2003US-0478742P
2003US-0478742P
2003US-0498529P
2003US-04991156P
2003US-0499154P
2003US-0499594P
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                                                                                                                                                                               100.0%;
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                                                                                                                                                                            Score 3079; DB 8 Pred. No. 1e-278;
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19-DEC-2000;
20-DEC-2000;
09-JAN-2001;
30-JAN-2001;
06-FEB-2001;
19-MAR-2001;
04-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  wound healing disorders; atherosclerosis; Parkinson's disease; Alzheimer's disease; autoimmune disorder; haematopoietic disorder; inflammation; neoplastic disease; nervous system disorder; cardiovascular disorders; pancreatitis; respiratory disorder; cardiovascular disorders; pancreatitis; respiratory disorder; hyper-immunity; developmental abnormality; gastrointestinal ulceration; neuropathy. haematological disease; metabolic disease; sperm dysfunction; thyroid disorder; hypothyroidism; brain damage; colitis; cone photo- transduction deficiency; neurological disease; stroke; angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart traches; thymus; lymph node; muscular system; obesity; anorexia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytostatic; vulnerary; antiarteriosclerotic; antiparkinsonian; nootropic; neuroprotective; immunosuppressive; haemostatic; antiinflammatory; cardiant; antiulcer; virucide; antithyroid; cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PALITARYHRDAGAPVYFYEFRHRPQCFEDTKÞAFVKADHADEVRFVFGGAFLKGDIVMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APEILSGSNKSLALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KPSKELLTLSQKTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LILS PMAKGLFHKA IMESGVA I I PYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVDFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFCAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGVSEDCLYLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGATEBEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APETLSGSNKSLALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVV
2000US-0256710P.
2000US-0257048P.
2001US-0260482P.
2001US-0264922P.
2001US-0264922P.
2001US-026797P.
2001US-0276988P.
2001US-0281535P.
                                                                                                                                                                                                                           2001WO-US049232.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 precocious puberty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gland; heart;
anorexia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neuropathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              540
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372

LALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRD

KTKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLPMKEAPBILSGSNKS HKAIMESGVAII PYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQ HKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQ WDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLF WDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLF IYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTT 191

365

311

251

185

245

305

S 밁 δ 밁 δ 밁 S 문 S

14 WAIWVLAAP-----TKGPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAP

65

WCFFLILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPPAAP

PLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHMLKVHYPKFGVSEDCLYLN 131

125

72

Best Local Sim Matches 553; Query Match

Similarity

94.7%; Score 2915; DB 5; 97.0%; Pred. No. 2.3e-263; tive 3; Mismatches 6;

9

8

Length

575;

Conservative

12

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The invention relates to an isolated polypeptide with signal sequences CC which allow it to be secreted extracellularly or membrane associated. The CC extentatic, vulnerary, antiarteriosclerotic, antiparkinsonian, notropic, cryostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, notropic, cardiant, antiulcer, virucide, antityroid, cerebroprotective, amorectic, CC endetabolic. Polypeptides and polynucleotides of the invention are CC useful in the treatment, or as a vaccine in the prevention of, cancer, CC wound healing disorders, infection, atherosclerosis, Parkinson's disease and Alzheimer's disease, autoimmune disorder, haematopoietic disorder, inflammation, neoplastic diseases, nervous system related disorders and CC hyperproliferation, systemic autoimmune disease, hyper-immunity, CC developmental abnormality, gastrointestinal ulceration, neuropathy, cancers e.g. hypothyroidism, brain damages, colitis, cone photocransity of the provention deficiency, neurological diseases, streke, angiogenesis, covulation deficiency, neurological diseases, streke, angiogenesis, CC ovulation of sorders, and alleviation of precocious puberty. The CC growth abnormalities, and alleviation of precocious puberty. The ccc growth abnormalities, and alleviation of precocious puberty. The ccc growth abnormality and the spinal cord, thyroid human of the invention
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(SMIK )
Sequence 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1(a); Page 312-313; 335pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAY-2001; 2001US-0289622P.
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¬η SA,
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SMITHKLINE BEECHAM
GLAXO GROUP LTD.
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A, Rizvi SK,
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Smith RF, Strum JC,
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Q;
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ARESULT 4
AAE25025
ID AAE2
XX AAE2
XX AAE2
XX JOO
XX Huma
XX Huma
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XX Huma
XX Huma
XX Arana
XX Doma
FT Doma
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          Sanjanwala MM, Yao
Lee EA, Ding L, H
Lal PG, Warren BA,
                                                                                                                                                    08-DEC-2000; 2000US-0254308P.
15-DEC-2000; 2000US-0256189P.
21-DEC-2000; 2000US-0257713P.
19-JAN-2001; 2001US-0267706P.
02-FEB-2001; 2001US-0266020P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; drug metabolising enzyme; autoimmune; inflammatory disorder; acquired immunedeficiency syndrome; AIDS; atherosclerosis; psoriasis; proliferative disorder; arteriosclerosis; clirchosis; hepatitis; cancer; asthma; neurological disorder; Alzheimer's disease; Huntington's disease; dementia; Parkinson's disease; developmental disorder; anaemia; adenoma; creal; screening; endocrine disorder; conjunctivitis; glaucoma; cataract; renal tubular acidosis; eye disorder; epilepsy; thrombosis; peptic ulcer; anorexia; metabolic disorder; cystic fibrosis; diabetes; liver disorder; goitre; gastrointestinal disorder; gene therapy; virucide; anticoagulant; anticonvulsant; nootropic; enzyme; DME-10.
                                                                                                                                                                                                                                                                                                        04-DEC-2001; 2001WO-US047429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE25025 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILSASDMLHSPLSSLTFLSLLQPFFFFFCAP
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Yao MG, Au-Young J, Bau
,, Hafalia AJA, Tang YT,
1 BA, Yang J, Walia NK,
                                                                                                          GENOMICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note=
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.56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Transmembrane domain'
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Baughn MR, Ar
YT, Yue H, Tr
NK, Nguyen DB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain'
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     Arvizu C,
Tribouley
DB, Gandhi
     £ 9
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  달
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WHI; 2002-519668/55.

DR WPGSD; AAD40574.

XX

WPI; 2002-519668/55.

DR N-PSDB; AAD40574.

XY

Novel human drug metabolizing polypeptide, useful in diagnosis, prevention or treatment of autoimmune/inflammatory, cell proliferative, prevention or treatment of autoimmune/inflammatory, cell proliferative, prevention or treatment of autoimmune/inflammatory, cell proliferative, prevention or treatment of autoimmune/inflammatory cell proliferative, and isocated human drug metabolic and gastrointestinal for disorders.

CC The invention relates to an isocated human drug metabolising enzyme (DME) and its nucleotide. DME is useful for disposing, treating or preventing cell disorders associated with aberrant expression of DME, where the disorders are selected from autoimmune/inflammatory disorder such as arteriosclerosis, psociasis, cell proliferative disorder such as arteriosclerosis, psociasis, uveitis; a cell proliferative disorder such as arteriosclerosis.

CC cinthosis, hepatitis, and cancer; a neurological disorder such as a neurological disorder such as endocrine disorder; an eurological disorder such as endocrine disorder such as renal tubular acidosis, epilepsy, can eye disorder such as conjunctivitis, glaucoma, cataract; metabolic cell disorder such as cystic fibrosis, diabetes and goitre; a gastrointestinal cell services such as anorexia, peptic ulcer; and liver disorders. DME is useful in a number of drug screening techniques and to analyse the conjunctivitis, glaucoma, cataract; metabolic cell such as anorexia, peptic ulcer; and liver disorders. DME is useful in a number of drug screening techniques and to analyse the construction due to translocation, inversion, etc. among normal, carrier or cell such as a such as anythidisation probes for mapping naturally cocurring genomic sequences. The present sequence is human DME-10 occurring genomic sequences. The present sequence is human DME-10
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Ś 밁 Ś 망 Ś 밁 ঠ 문 S 밁 S 밁 S В Ś 밁 5 Matches Query Match Best Local (451 452 391 392 331 332 271 211 151 152 548; 31 GPSAEGPORNTRIGWIQGKQVTVIGSSPVPVNVFLGVPFAAPPLGSIRFTNPQPASPWDNL 92 DLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIPLILSASDMLHSPLSSLTFLS Similarity TKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEBKLLSRKMMKYWATFARTGNPNGN VANEYFHDKHSITEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFED VANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFED DLLSQKAFKAIPSIIGVNNHECGFLLPMKEAPEVLSGSNKSLALHLIQNILHIPPQYLHL DLLSQKAFKAIPSIIGVNNHECGFLLPMKEAPEILSGSNKSLALHLIQNILHIPPQYLHL WVQKNIEFFGGDPSSYTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIPYLEAHD 270 PGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALS 210 REATSYPNICLONSEWILLDOHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWF REATSYPNICLQNSEWILLIDQHMLKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWF 150 YEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEPL YEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFENEPL 330 WVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIPYLEAHD PGGAFKTGSAS I FDGSALAAYEDVL VVVVQYRLG I FGFFTTWDQHAPGNWAFKDQVAALS GPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAPPLGSLRFTNPQPASPWDNL Conservative 94.2%; 2; Score 2900; DB 5 Pred. No. 7e-262; 2; Mismatches DB 5; Length Indels 0, Gapa 570 510 511 450 451 391 331 211 151

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RESULT 5
ABM84114
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                                               The invention relates to novel diagnostic and therapeutic polynucleotides CC selected from one of the 2722 sequences defined in the specification. A CC polynucleotide of the invention may have a use in gene therapy. The human CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated CC with human molecules, e.g. cell proliferative disorders, condition for the proliferative disorders, conditions caused by virus, bacteria, fungion parasite. The dithp CC disorder, neurological disorders, gastrointestinal disorders, or CC infections caused by virus, bacteria, fungion parasite. The dithp CC molecules may also be used in genetic mapping, in identifying individuals CC from minute biological samples, in detecting single nucleotide CC polymorphisms, as molecular weight maxiers, and for somatic or germline CC gene therapy. The present sequence represents a dithp protein of the convention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly forms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F; Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV; Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP; Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL; Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Giventury S, Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                  New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gietzen D;
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Query Match Best Local Similarity

94.2%;

Score 2900; DB 8; Pred. No. 7e-262;

Length 642;

WO200250105-A1 Homo sapiens.

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                                                                                                                                                                   cone photo- transduction deficiency; neurological disease; stroke; angiogenesis; ovulation disorder; spinal cord; thyroid gland; hear trachea; thymus; lymph node; muscular system; obesity; anorexia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytostatic; vulnerary; antiarteriosclerotic; antiparkinsonian;
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Best Local Similarity 91.4%;
Matches 499; Conservative
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20-DEC-2000; 2000US-0257048P.
09-JAN-2001; 2001US-0264922P.
30-JAN-2001; 2001US-0264922P.
06-FEB-2001; 2001US-0266979P.
19-MAR-2001; 2001US-0276988P.
04-APR-2001; 2001US-0289622P.
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Martensen (
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Parkinson's
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WDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLF
                                               ŢĀPĀHĀDTGSKLPVLVWFPGGĀFKTGSĀSIFDGSĀLĀĀVEDVLVVVVQYRLGIFGFFTT
                                                                   IYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVQXRLGIFGFFTT
                                                                                                              PLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHMLKVHYPKFGVSEDCLYLN
                                                                                                                                  PLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHMLKVHYPKFGYSEDCLYLN
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SMITHKLINE BEECHAM PLC.
GLAXO GROUP LTD.
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                                                                                                                                                                                          WCFFLILOPLLGHROWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteins and polynucleotides useful as vaccines for preventing ing various diseases e.g. cancer, wounds, atherosclerosis, n's disease, Alzheimer's disease, infection, autoimmune disorder.
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A, Rizvi SK,
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Smith RF,
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                                                                                                                                                                                                                                               Score 2607.5; DB 5;
Pred. No. 1.4e-234;
7; Mismatches 25;
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, Strum JC,
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                                                                                                                                                                                                                                                                                                                                                                    Isogai T, Si
                                                                                                                                                                        New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease.
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24-JAN-2002; 2002US-0350435P.
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DB; ADA53168.
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RES ASSOC BIOTECHNOLOGY.
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J, Isono Y,
Yoshikawa T,
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Hio Y, Otsuka K, Nagai
Otsuka M, Nagahari K, N
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K, Irie
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ho Y;
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The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.

Claim 14; SEQ ID NO 2375; 205pp; English.

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2001US-03124802P.
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2001US-0332131P.
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2001US-03321779P.
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CURAGEN CORP.

Guo X, Kekuda R, Miller CE, Malyankar UM, Spytek KA;
Patturajan M, Liu X, Gusev VY, Li L, Vernet CAM, Zerhusen BD
Gorman L, Shenoy SG, Pena CEA, Smithson G, Burgess CE, Gerla
Padigaru M, Shinkets RA, Gangolli EA, Taupler RJ, Casman SJ,
Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ;
Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA; Ellerman K; Spytek KA; et CAM, Zerhusen BD;

WPI; N-PSDB; 2003-046858/04. ABX72267.

New isolated NOVX polypeptide useful for treating atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease and cancer.

Claim Ļ Page 303; 666pp; English.

The invention relates to human polypeptides, termed NOVX, and the polypucleotides encoding them. The polypeptides and polynucleotides are useful for diagnosing disease, and screening for potential therapeutic agents. The sequences are useful for treating metabolic disorders, cardiomyopathy, diabetes, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD), atrioventricular canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, immune disorders, haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease and cancer. Sequences ABU54542-ABU54647 represent human NOVX polypeptides of the invention

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    29-SEP-2000;
06-OCT-2000;
20-OCT-2000;
09-NOV-2000;
16-NOV-2000;
                                                                                                                                                                                                                                                                                                                              drug metabolising enzyme; DME; cytostatic; immunosuppressive; antiinflammatory; endocrine; ophthalmological; gastrointestinal; hepatotropic; cancer; cell proliferative disorder; autoimmune di inflammatory disorder; endocrine disorder; eye disorder; gastrointestinal disorder; liver disorder; metabolic disorder; e
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497; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 metabolising enzyme
; 2000US-0236947P.
; 2000US-0238864P.
; 2000US-0242323P.
; 2000US-0247581P.
; 2000US-0247581P.
                                                                                                                                   2001WO-US030662
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1; Mismatches
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No. 1.2e-233;
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DLLSQKAFKAIPSIIGVNNHECGFLLPM-----

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DLLSQKAFKAIPSIIGVNNHECGFLLPMKEAPEILSGSNKSLALHLIQNILHIPPQYLHL YEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEPL

YEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEPL

WVQKNIEFFGGDPSSVTIFGBSAGAISVSSLILSPMAKGLFHKAIMESGVAIIPYLEAHD

TKPAFVKADHADEVRFVFGGAFLKGDIVMFBGATEEEKLLSRKMMKYWATFARTGNPNGN

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                                                                                                                                                                                                                                                                                                          cc rucleotide sequences which encode them. The invention may be useful for the development of compounds with a cytostatic, immunosuppressive, antiinflammatory, endocrine, ophthalmological, gastrointestinal or chepatotropic activity acting as an agonist or antagonist of drug cardinatestive of disorders associated with decreased in the diagnosis cardinates or activity of drug metabolising enzyme. Such disorders associated with decreased or increased capression or activity of drug metabolising enzymes. Such disorders conclude cancer, cell proliferative disorders, autoimmune/inflammatory, condocrine, eye, gastrointestinal (including liver disorders) and cometabolic disorders. The present sequence is that of a human drug metabolising enzyme (DME) of the invention. Note: This sequence did not compart of the printed specification but was obtained in electronic compart from EPO.
                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Azimzai Y, Baughin MR, Bo
Bliott VS, Gandhi AR, Gj
Lal P, Lee EA, Lu DAM, N
Ring HZ, Sanjanwala MS, T
Walsh RT, Warren BA, Xu Y
                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 2; 142pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human drug metabolizing enzymes, useful disorders associated with aberrant (DME) autoimmune disorders.
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N-PSDB; ADR19681.
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30-NOV-2000;
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                                                                                                       152
                                                                                                                                                                                                                          491;
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WVQXNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIFYLEAHD
                                                                                                 REATSYPNICLQNSEWILLIDQHMIKVHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWF
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                                       PGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALS
                                                        PGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALS
                                                                                                                REATSYPNICLONSEWILLIDOHMIKVHYPKFGVSEDCLYINIYAPAHADTGSKIPVIVWF
                                                                                                                                                                                                                                                                                     618
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2000US-0250567P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borowsky ML, Ding L, Duggan BM;
Griffin JA, Hafalia AJA, Ison CH,
Nguyen DB, Arvizu C, Policky JL,
Tang YT, Tribouley CM, Narinder 1
1 Y, Yang J, Yao MG, Yue H;
                                                                                                                                                                                                                     ; Score 2588.5; pred. No. 9.6e. 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                     5; DB 5;
).6e-233;
les 5;
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e H;
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                                                                                        The invention discloses a polynucleotide comprising a sequence selected CC from 1970 fully defined nucleotide sequences which encode novel CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, an antibody binding to the polypeptide or peptide CC of the polynucleotide, immunologically assaying the polypeptide or peptide CC with the antibody of the encoded protein, and observing the binding CC between the two, a transformant carrying the polypeptide or peptide CC with the antibody of the encoded protein, and observing the binding CC expressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide or as a probe CC for detecting the polynucleotide. The polynucleotide core detecting the polynucleotide. The polynucleotide of genes may be included in them, for developing a diagnostic marker or CC medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell cranscription-related proteins, signal transduction-related proteins, currously them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence data for this patent is not represented in the printed corection but is based on sequence information supplied by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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25-JAN-2002; 2002US-00350978.
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DB; ADB62095.
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Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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Sequence 469 AA;

Patent Office.

The present sequence represents a cat cauxin protein (I) or its salt, which is cat kidney disease marker. Also described: (1) a partial peptide (II) of (I); (2) a nucleic acid (III) encoding (I) or (II); (3) a vector

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RESULT 11
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Matches 467
                                                                                                                                                Novel cauxin protein or its salt, useful and for diagnosing cat kidney disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cat; cauxin;
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                                                                                                  Claim 3;
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                                                                                                ID NO 2; 33pp; Japanese.
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Pred. No. 2.4e-220;
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Best Local Similarity
Matches 373; Conser
                                JP2003250575-A
                                                                                                                                                                                                                                      12-FEB-2004
                                                                                                                                                                                                                                                                                        ADF50147
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                                                                                                                                                                                                                                                                                                                                           ADF50147
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                                                                                                                                                                                cauxin protein SEQ ID NO:4.
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                                                                                                                                                                                                                                                                                                                                         standard;
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                                                                                                                             kidney disease
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                                                                                                                                                                                                                                                                                                                                         542
                                                                                                                             marker;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a cat cauxin protein (I) or its salt, (C which is cat kidney disease marker. Also described: (I) a partial peptide (II) of (I); (2) a nucleic acid (II) encoding (I) or (II); (3) a vector (C (IV) comprising (III); (4) a transformed host (V) comprising (III) or (C (IV); (5) producing (I) or (II) by culturing (V); (6) a antibody (VI) (C (IV); (5) producing (I) or (II); (7) diagnosing cat kidney (C (IV); (6) a cat kidney (IV) or (IV); (7) diagnosing cat kidney (IV) or (IV); (8) a cat kidney (IV) or (IV); (9) a cat kidney (1V) comparison (IV); (1V); (1V); and where reduction (C (IV); (1V); and (IV); an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local :
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DTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATBEEKLLSRKWMKYWATFARTGNPNG 509
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                                                                                                                    LVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEFRHRPQCFE
                                                                                                                                                                               VALLTOKAFNSVPSIIGVNNHECAFLL-STEFSEILGGSNRSLALYLVHTFLNIPTQYLH
                                                                                                                                                                                                       LDLLSQKAFKAIPSIIGVNNHECGFLLPMKEAPEILSGSNKSLALHLIQNILHIPPQYLH 389
                                                                                                                                                                                                                                                                         GDERKKDLQVLARICGCHASDSAALLQCLRAKPSEELMDISKKLTFSIPVIDDFFFPDEP
                                                                                                                                                                                                                                                                                                           DYEKSEDLQVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGAFFPNEP
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                                                                                          LVADHYFYNKHSPVEIRDSFLDLLGDVLFVVPGVVTARYHRDAGAPVYFYEFQHPPQCLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.5%; Score 1985; DB 8; 71.7%; Pred. No. 2.4e-176; tive 60; Mismatches 85;
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EGVPLWPAYTQSEQYLKLDLSVSVGQKLKEQEVEFWMNTI 540

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KW nootropic; neuroprotective; immunosuppressive; haemostatic;
KW nootropic; neuroprotective; immunosuppressive; haemostatic;
KW drifinflammatory; cardiant; antiulcer; virucide; antithyroid;
KW cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
KW wound healing disorders; atherosclerosis; parkinson's disease;
KW vound healing disorders; atherosclerosis; parkinson's disease;
KW vound healing disorders; autoimmune disorder; harminopoietic disorder;
KW liflammation; neoplastic disease; nervous system disorder;
KW cardiovascular disorders; pancreatitis; respiratory disorder;
KW developmental abnormality; gastrointestinal ulceration, neuropathy;
KW developmental abnormality; gastrointestinal ulceration; neuropathy;
KW haematological disease; metabolic disease; sperm dysfunction;
KW haematological disease; metabolic disease; sperm dysfunction;
KW thyroid disorder; hypothyroidism; brain damage; colitis;
KW cone photo- transduction deficiency; neurological disease; stroke;
angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;
KW traches; thymus; lymph node; muscular system; obesity; anorexia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-2000;
20-DEC-2000;
09-JAN-2001;
30-JAN-2001;
06-FEB-2001;
The invention relates to an isolated polypeptide with signal sequences which allow it to be secreted extracellularly or membrane associated. The activity of polypeptides of the invention may be described as, cytostatic, vulnerary, antiarteriosclerotic, antiaparkinsonian, nootropic, neuroprotective, immunosuppressive, haemostatic, antiinflammatory, cardiant, antiuleer, virucide, antithyroid, cerebroprotective, anorectic, and metabolic. Polypeptides and polynucleotides of the invention are useful in the treatment, or as a vaccine in the prevention of, cancer, wound healing disorders, infection, atherosclerosis, Parkinson's disease and Alzheimer's disease, autoimmune disorder, haematopoietic disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agarwal P,
Martensen 9
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                                                                                                                                                                                                                                                                                                                                                           Claim 1(a); Page 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
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(SMIK )
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2001US-0264922P.
2001US-0266797P.
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rum JC, Xie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 osteopathic; gene therapy; osteoporosis; detoxifying agent; Paget's disease; bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE20911;
                                                                                  (FARB )
                                                                                                                                       17-JUL-2000; 2000US-0218564P
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100.0%; Pred. No. 2e-157;
Live 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       antisense therapy; cytostatic; implant degradation; cancer;
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CC screening for agents which decrease or modulate the activity of carboxylesterase-like enzyme polypeptide. Carboxylesterase-like enzyme is useful for treating a carboxylesterase-like enzyme dysfunction related consease, such as organophosphorus intoxication, cancer and osteoporosis. Compounds that increase the ability of human carboxylesterase-like enzyme to bind to organophosphorus compounds are useful as detoxifying agents. Carboxylesterase-like enzyme agonists and antagonists are useful for treating osteoporosis, paget's disease and degradation of bone implants. Carboxylesterase-like enzyme is useful in garticularly dental implants. Carboxylesterase-like enzyme is useful in susceptibility to diseases or abnormalities related to the presence of coding sequence of carboxylesterase-like enzyme polynucleotide is useful in gene therapy and for generating antisense oligonucleotides or carboxylesterase-like enzyme by much specifically bind to mRNA transcribed from carboxylesterase-like enzyme gene expression. The necessary carboxylesterase-like enzyme gene expression. The necessary carboxylesterase-like enzyme gene expression. The necessary carboxylesterase-like enzyme gene expression. The necessary carboxylesterase-like enzyme gene expression. The necessary carboxylesterase-like enzyme gene expression. The necessary expression is the necessary expression are necessary expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 VHYPKFGVSEDCLYLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVL 175
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LDLNMSLGQRLKEPRVDFWTSTIP 550
                                                                         VF-GSFFSGMKLDF---TEEERLLSRRNMKYWANFARQGNPNSEGLPYWPALDHDEQYLQ
                                                                                                                                                                                                                                                                                                 TIPMVMGTAQIIKE----LSRENLQAVLKDTAAQMMLPPECGDLLMEEYMGNTDDSQTLQ
                                                                                                                   VFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQ 526
                                                                                                                                                                                       DSLLDLLGDVFFVVPALITARYHRDAGAFVYFYBFRHRPQCFEDTKPAFVKADHADEVRF
                                                                                                                                                                                                                                                                                                                                                      LLPM-----KEAPEILSGSNKSLALHLIQNILHIPPQYLHLVANEYFHDKHSLTEIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVVVQYRLGIFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGA
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Pred. No. 1.1e-108;
7; Mismatches 179;
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Sequences AAF21614 - AAF22031 represent DNA sequences encoding human C proteins AAB59111 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the CC invention. The breast and ovarian cancer associated DNA, protein, agonist corrective, antiviral; antiallergic; hepatotropic; antidiabetic; cneuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiparasitic and cardiant activity. The polynucleotide and CC protein sequences are used in the diagnosis of cancer, particularly CC antifungal; antiparasitic and cardiant activity. The polynucleotide and CC protein sequences are used in the diagnosis of cancer, particularly CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment CC fimmune disorders e.g. Addison's disease, allergies, autoimmune CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; cardiovascular diseases such as cerebral anoxia and epilepsy; and cinfertions diseases such as cerebral anoxia and epilepsy; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
AAB58981
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 1142-1144; 1299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatme and diagnosis of cancer, immune disorders, cardiovascular disorders are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; noctropic; neurpprotective; antiviral; antiallergic; hepacotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant, antibacterial; antifungal; antiparasitic; cardiant; immune disorder; addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-2000; 2000WO-US005881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Breast and ovarian cancer associated antigen protein sequence SEQ ID 689.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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GPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAPPLGSLRFTNPQPASPWDNL

Matches 248;

Conservative

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Score 1230; DB 3; Pred. No. 1.2e-105;)1; Mismatches 168;

Length 549; Indels

24;

Gaps

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Query Match Best Local

Local Similarity

39.98;

Sequence 549 infectious diseases

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US-09-595-682B-28
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APPLICANT: Dotter, Philip M.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth (
TITLE OF INVENTION: Tumor Cells
FILE REFERENCE: SJ-0005
CURRENT APPLICATION NUMBER: US/09/595,682B
CURRENT FILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: 60/075,258
PRIOR APPLICATION NUMBER: 60/075,258
PRIOR APPLICATION NUMBER: PT/US99/03171
PRIOR APPLICATION NUMBER: PT/US99/03171
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 559
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ORGANISM: Homo
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                                                                                    FFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLP----MKEAPEILSGSNKSLALHLIQN
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTER, J. CRAIG et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES

FILE REFERENCE: CLOO1307

CURRENT ETLING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-08

JENIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

JENIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

JENIOR                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LENGTH: 559
; TYPE: PRT
; ORGANISM: Human
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                             EFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEBEKLLGRKMMKYWA 499
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46.7%; Pred. No. 4.8e-125;
ative 91; Mismatches 168;
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FILE REPERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR RILING DATE: 2000-10-03

PRIOR PILICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER: OF SEQ ID NOS: 207012

SOFTWARE: FRASUSEQ for Windows Version 4.0

SEQ ID NO 9670

LENGTH: 577

TYPE: PRT

ORGANISM: Human

US-09-949-016-9670
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Best Local S
Matches 248
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Sequence 9670, Application US/09949016

Patent NO. 6812339

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                  BFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMKKYWA 499
                                                                                                                                                                                                                                                                                                                            VAALSWVQXNIEFFGGDPSSVTIFGESAGAISVSSLILSPMAKGLFHKAIMESGVAIIPY 265
                                                                                                                                                                                                                                                                                                                                                                     GQDSASPIRTTHTGQVLGSLVHVKGANAGVQTFLGIPFAKPFLGFLRFAPPEPESWSGV
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LIMIPPTFGDLLRERYIGDNGDPQTLQAQFQEMMADSMFVIPALQVAHF-QCSRAPVYFY
                                                                                                                                                     ILHIPPOYLHLVANEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFY
                                                                                                                                                                                                   PFPNEPLDLLSQKAFKAIPSIIGVNNHECGFLLP----MKEAPEILSGSNKSLALHLIQN
                                                                                                                                                                                                                                                                LEAHDYEKSEDL--QVVAHFCGNNASDSEALLRCLRTKPSKELLTLSQKTKSFTRVVDGA
                                                                                                                                                                                                                                                                                                          VAALRWVQQNIAHFGGNPDRVTIFGESAGGTSVSSLVVSPISQGLFHGAIMESGVALLPG
                              TFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIP 550
                                                            EFQHQPSWLKNIRPPHMKADHGDELPFVF~RSFFGGNYIKF~~~TEEBEQLSRKMMKYWA
                                                                                                                                                                                   FLPRHPQELLASADFQPVPSIVGVNNNEFGWLIPKVMRIYDTQKEMDREASQAALQKMLT 395
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RESULT 5 US-09-595-682B-21

RESULT 6
US-09-264-737-2
IS-09-264-737-2
; Sequence 2, Application US/09264737A
; Patent No. 6107549
; GENERAL INFORMATION:

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APPLICANT: Danks, Mary K.
APPLICANT: Potter, Philip M.
APPLICANT: Houghton, Peter J.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Tumor Cells
FILE REPERENCE: SJ-0005
CURRENT APPLICATION UNMBER: US/09/595,682B
CURRENT FILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: 60/075,258
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR FILING DATE: 1999-02-12
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LENGTH: 565
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POWPAYDYKEGYLQIGATTQAAQKLKDKEVAFWT 547
                                  SIMPAYNLTEQYIQLDLNMSLGQRLKEPRVDFWT 546
                                                                                                                                               EKYLGGTDDPVKKKDLFLDMLADLLFGVPSVNVARHHRDAGAPTYMYEYRYRPSFSSDMR
                                                                                                                                                                                                                                                         VNNHECGFLLPM------KEAPEILSGSNKSLALHLIQNILHIPPQYLHLVA 392
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                                                                       PKTVIGDHGDEIFSVLGAPFLK-----EGATEEEIKLSKMVMKYWANFARNGNPNGEGL
                                                                                                          PAFVKADHADBVRFVFGGAFLKGDIVMFEGATBEEKLLSRKMKYWATFARTGNPNGNDL
                                                                                                                                                                                                                                                                                                                                                                         SPLTKNLFHRAISESGVALLSSL----FRKNTKSLAEKIAIEAGCKTTTSAVMVHCLRQK
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43.9%; Pred. No. 2.5e-116;
rative 75; Mismatches 180;
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RESULT 7

US-09-595-682B-26

Sequence 26, Application US/09595682B

PATENT NO. 6800483

GENERAL INFORMATION:

APPLICANT: Danks, Mary K.

APPLICANT: Houghton, Peter J.

TITLE OF INVENTION: Compositions and I TITLE OF INVENTION: Tumor Cells

TTTE OF EFFERENCE: SJ-0005
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APPLICANT: Ruff, Thomas G.

TITLE OF INVENTION: Engineering Plant Resistance to Pyridines via TITLE OF INVENTION: Expression of Esterase Enzymes

FILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance CURRENT APPLICATION NUMBER: US/09/264,737A

CURRENT FILING DATE: 1999-03-09

EARLIER FILING DATE: 1999-03-10

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 566

TYPE: PRT

TYPE: PRT
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US-09-264-737-2
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Best Local Similarity 43.6%;
Matches 250; Conservative 7:
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Pred. No. 5.16
                                          Methods for Sensitizing
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5.1e-115;
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CURRENT APPLICATION NUMBER: US/09/595,682B;
CURRENT FILING DATE: 2000-01-16;
PRIOR APPLICATION NUMBER: 60/075,258;
PRIOR FILING DATE: 1998-02-19;
PRIOR APPLICATION NUMBER: PCT/US99/03171;
PRIOR FILING DATE: 1999-02-12;
NUMBER OF SEQ ID NOS: 30;
SOFTWARE: Patentin Ver. 2.0;
SEQ ID NO 36
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TYPE: PRT
ORGANISM: Oryctolagus cuniculus
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                                                                                                                                                                         NEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAFVYFYEFRHRPQCFEDTK 452
POWPAYDYKEGYLÓIGATTQAAQKLKDKEV
                                                                   PKTVIGDHGDEIFSVLGAPPLK-----EGATEEEIKLSKWVMKYWANPARNGNPNGEGL
                                                                                         PAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWATFARTGNPNGNDL 512
                                                                                                                                             EKYLGGTDDPVKKKÖLFLÖMLADLLFGVPSVNVÄRHHRDÄGÄPTYMYEYRYRPSFSSÖMR
                                                                                                                                                                                                                                                         VNNHECGFLLPM------KEAPEILSGSNKSLALHLIQNILHIPPQYLHLVA 392
                                                                                                                                                                                                                                                                                              TEEBLMEVTLKMKFMALDLVGDPKENTAFLTTVIDGVLLPKAPAEILAEKKYNMLPYMVG
                                 SLWPAYNLTEQYLOLDLNMSLGQRLKEPRV 542
                                                                                                                                                                                                                     INQQEFGWIIPMQMLGYPLSEGKLDQKTATELLWKS-----YPIVNVSKELTPVAT
                                                                                                                                                                                                                                                                                                                                  PSKELL--TLSQK-----TKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIG
                                                                                                                                                                                                                                                                                                                                                                      SPLTKNLFHRAISESGVALLSSL----FRKNTKSLAEKIAIEAGCKTTTSAVMVHCLROK
                                                                                                                                                                                                                                                                                                                                                                                                            SPMAKGLFHKAIMESGVAIIPYLEAHDYEKSED--LQVVAHFCGNNASDSEALLRCLRTK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                ĠĨWĠFFSTGDEHSRĠNWGHLDQVAALRWVQDNIANFGGDPGSVTIFGESAGGQSVSILLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEDCLYLNIYAPAHADTGSKLPVLVWPPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WCFFLILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLGSLRFTNPQPASPWDNLREATSYPNLCLQNSEWLLLDQHML-----KVHYP-KFGV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75; Mismatches
543
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US-08-45-295A-2
; Sequence 2, Application US/08845295A
; Patent No. 5817490
; Patent No. 5817490
; Patent No. TITLE OF INVENTION: Enzymatic Process for the Manufacture of TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and TITLE OF INVENTION: 2-Keto-L-Gulonic Acid, and NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: Bastman Chemical Company STREET: P.O. Box 511
; CITY: Kingsport
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Esters

COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch disk

37662-5075

Tennessee

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COMPUTER: ISM COMPATION:
OPERATING SYSTEM: Windows 95
SOPTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,295A
FILING DATE: 25-April-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,879
FILING DATE: 17-MAX-1996
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70432
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: Amino Acid
TYPE: Amino Acid
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nes 259; Conserv
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                                                                                                                                                                                          YLHLVANBYFHDKH-----SLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYEF 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---SEDCLYLNIYTPADLTKRGRLPVMVWIHGGGLVLGGAPMYDGVVLAAHENFTVVVVA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FGVSEDCLYIMIYAPAHADTGSKLFVLVWFPGGAFKTGSASIFDGSALAAYED--VLVVV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KPPLGSLRFAPPQPABPWSFVKNTTSYPPMCCQDPVVEQMTSDLFTNFTGKERLTLEF-- 117
AIPSIIGVNNHECGPLLP-------MKEAPEILSGSNKSLALHLIQNILHIPPQ 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VQYRLGIFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGES--AGAI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLGSLRFTNPQPASPWDNLREATSYPNLCLQNS--EWLLLD------QHMLKVHYPK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WCFFLILQPLLGHRQWGKTGFSAEGFQRNTRLGWIQGKQVTV--LGSFVFVNVFLGVFFA 69
                                                                                 QYRPSFSSDKFTKPKTVIGDHGDEIFSVFGFPLLKGD-----APEEEVSLSKTVMKFWA
                                                                                                                       RHRPQCFED--TKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMKYWA 499
                                                                                                                                                                                                                                             TVPYIVGINKQEFGWLLPTWYGFPLSEGKLDQKTATSLLWKS-----YPIANI----PE
                                                                                                                                                                                                                                                                                                                                   CLRQKSEDELLDLTLKMKFLTLDFHGDQRESHPFLPTVVDGVLLFKMPEEILAEKDFTFN 354
                                                                                                                                                                                                                                                                                                                                                                       SVSVLVLSPLAKNLFHRAISESGVALTVALVRKDMKAAAKQIAVLAGCKTTTSAVFTFVH 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WILLPLVITSLASSATW--AGQPASPPVVDTAQGRVLGKYVSLEGLAFTQPVAVFLGVPFA
                                      TFARTGNPNGNDLSLWP--AYNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTI 549
                                                                                                                                                                  ELTPVAT--PTDKYLGGTDDPVKKKDLFLDLMGDVVFGVPSVTVARQHRDAGAPTYMYEF
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43.8%; Pred. No. 7.4e-110;
ative 63; Mismatches 191; Indels 79;
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RESULT 9
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,879; 08/845,295
APPLICATION NUMBER: US 60/017,879; 08/845,295
FILING DATE: 17-May-96; 25-April-97
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70432
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 423-229-6189
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Best Local (
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Hubbs, John C.
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TITLE OF INVENTION: ASC.
TITLE OF INVENTION: 2-K.
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US,
FILING DATE: 27-August-
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 584 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 35.4%; Score 1091.5; DB 3; Local Similarity 43.8%; Pred. No. 7.4e-110;
295
                                                                     297
                                                                                                                                                                                                                                                                                                                                                179 VQYRLGJFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGES--AGAI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGVSEDCLYLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYED--VLVVV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KPPLGSLRFAPPQPAEPWSFVKNTTSYPPMCCQDPVVEQMTSDLFTNFTGKERLTLEF--
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                                                                     CLRTKPSKELLTLSQKTKSFT-------RVVDGAFFPNEPLDLLSQK--AFK 339
CLRQKSEDELLDLTLKMKFLTLDFHGDQRESHPFLPTVVDGVLLPKMPEEILAEKDFTFN 354
                                                                                                                                                                                                                             SVSSLILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSEDLQVVAHFCGNNASDSEALLR 296
                                                                                                                                                                                                                                                                                                           IQYRLGIWGFFSTGDEHSRGNWGHLDQVAALHWVQENIANFGGDPGSVTIFGESFTAGGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---SEDCLYLNÍYTPÄDLTKRGRÍPVMVWIHGGGLVLGGAPMYDGVVLAAHENFTVVVVA 174
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P.O. Box 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            บร/09/140, 933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 584;
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JENGTH: 584 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: protein
US-09-146-661-2
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US-09-146-661-2
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                                                                                                                                                                       Matches
                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,879; 08/845,295
FILING DATE: 17-May-96; 25-April-97
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70432
TELECOMMUNICATION INFORMATION:
TELEPHONE: 423-229-6189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                       TELEFAX: 423-229-1239
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09146661 Patent No. 6136575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/
FILING DATE: 03-Septmeber-
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hubbs, John C.
TITLE OF INVENTION: Enzymatic Process
TITLE OF INVENTION: Assorbic Acid, 2-K
TITLE OF INVENTION: Acid
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eastman Chemical Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 37662-5075
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Kingsport
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                                                                                                                                                                       259;
                                      70 APPIGSIRFTNPQPASPWDNLREATSYPNLCLQNS--EWLLLD------QHMLKVHYPK 120
                                                                                                                     12 WCFFLILQPLLGHRQWGKTGPSAEGPQRNTRLGWIQGKQVTV--LGSPVPVNVFLGVPFA 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       442 RHRPQCFED--TKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWA 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              405 ELTPVAT--FTDKYLGGTDDPVKKKDLFLDLMGDVVFGVPSVTVARQHRDAGAPTYMYEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  387 YLHLVANEYFHDKH-----SLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVYFYBF
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                                                                                  WLLPLVLTSLASSATW--AGQPASPPVVDTAQGRVLGXYVSLEGLAFTQPVAVFLGVPFA
        KPPLGSIRFAPPOPAEPWSFVKNTTSYPPMCCODPVVEOMTSDLFTNFTGKERLTLEF--
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                                                                                                                                                                   Conservative
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                                                                                                                                                             ; Score 1091.5; DB 3; 
; Pred. No. 7.4e-110; 
63; Mismatches 191;
                                                                                                                                                               Indels
                                                                                                                                                                                                  Length 584;
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                                                                                                                                                             Gaps
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US-09-150-515-2
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                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/150,515
FILING DATE: 09-SEP-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,879; 08/845,295
FILING DATE: 17-May-96; 25-April-97
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70432
TELECOMMUNICATION INFORMATION:
TELEPHONE: 423-229-6189
TELEPHONE: 423-229-6189
TELEFAX: 423-22 IN NO. POR SEQ ID NO. PROJENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09150515
Patent No. 6271006
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                                                                                                                                                                                                                                                                                                                                                                          ZIP: 37662-5075
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Enzymatic Process
TITLE OF INVENTION: Ascorbic Acid, 2-F
TITLE OF INVENTION: 2-Keto-L-Gulonic F
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eastman Chemical Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kingsport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NFARSGNPNGEGLPHWPFTMYDQEEGYLQIGVNTQAAKRLKGEEVAFWNDLL 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RHRPQCFED--TKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWA 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELTPVÅT--FTDKYLGGTDDPVKKKDLFLDLMGDVVFGVPSVTVÅRQHRDÅGAPTYMYEF 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tennessee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IQYRLGIWGFFSTGDEHSRGNWGHLDQVAALHWVQENIANFGGDPGSVTIFGESFTAGGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VQYRLGIFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGES--AGAI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---SEDCLYLNIYTPADLTKRGRLÞVMVWIHGGGLVLGGAPMYDGVVLAAHENFTVVVVA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGVSEDCLYLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYED--VLVVV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P.O. Box 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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516

441 404 354

294

and

Esters

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; TOPOLOGY: Linear ; MOLECULE TYPE: protein US-09-150-515-2

TYPE: Amino Acid

Best Local Similarity 42.2%; Pred. No. 1.1e-103; Matches 234; Conservative 71; Mismatches 176;

Indels

73;

Gaps

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92

EATSYPNICLQNSEWILLDQHMI------KVHYP-KFGVSEDCLYINIYAPAHADTGSK 143

PSAP-PVVDTVKGKVLGKFVSLEGFAQPVAVFLGVPFAKPPLGSLRFAPPQPAESWSHVK PSAEGPQRNTRLGWIQGKQVTVLGSPVPVNVFLGVPFAAPPLGSLRFTNPQPASPWDNLR

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                                    US-09-264-737-1
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US-09-264-737-1
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                                                    SEQ ID NO 1
LENGTH: 539
TYPE: PRT
ORGANISM: Rabbit
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Feng, Paul C.C.
APPLICANT: Ruff, Thomas G.
                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09264737A Patent No. 6107549
Query Match
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                                                                                                                       TITLE OF INVENTION: Engineering Plant Resistance to Pyridines TITLE OF INVENTION: Expression of Esterase Enzymes FILE REFERENCE: 38-21 (10551) RLE3 Pyridine Tolerance CURRENT APPLICATION NUMBER: US/09/264,737A CURRENT FILING DATE: 1999-03-09 EARLIER APPLICATION NUMBER: 60/077,377 EARLIER FILING DATE: 1998-03-10 NUMBER OF SEQ ID NOS: 11 SOPTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
mes 259; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QYRPSFSSDKFTKPKTVIGDHGDEIFSVFGFPLLKGD----APEEEVSLSKTVMKFWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELTPVAT -- FTDKYLGGTDDPVKKKDLFLDLMGDVVFGVPSVTVARQHRDAGAPTYMYEF
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Pred. No. 7:4e-110;
3; Mismatches 191;
Score 1034.5;
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Length
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RESULT 13
US-08-446-100-26
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Broomileto,
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Okeana
APPLICANT: Lockridge, Okeana
APPLICANT: Site-Directed
                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                       STREET: 9669 A CITY: Fairfax STATE: VA
                                                                                                                                                                                                                            ZIP:
                                                                                                                                                                                                                                        COUNTRY: US
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9669 A Main Street, P.O.
                                                                                            US/08/446,100
                                                                                                                                #1.0,
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472 393 412 342 282 312 226

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; Sequence 28, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Obsana
; TITLE OF INVENTION: Site-Directed Mu
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
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US-08-446-100-28
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Best Local Similarity 44.9%; Pred. No. 9.5e-94;
Matches 200; Conservative 64; Mismatches 150
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HYPOTHETICAL: YES
ANTI-SENSE: YES
FRACMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: human esterases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
             STREET: 9669 A
CITY: Fairfax
STATE: VA
COUNTRY: US
ZIP: 22031
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                                                                                                           ADDRESSEE: Hendricks and Assoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 454 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTE 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELFSVFGAPFLK-----EGASEEEIRLSKMVMKFWANFARNGNPNGKGLPHWPEYNQKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NKQEFGWLIPMQLMSYPLSEGQLDQKTAMSLLGSPIPLFAIAKELIPEATEKYLGGTDDT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNHECGFLLPMKEAPEILSGS--NKSLALHLIQN---ILHIPPQYLHLVANEYFHDKHSL 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEELLETTLKIGNSYLWTYRETQRESTLLGTVIDGMLLLKTPEELQRERNFHTVPYMVGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PMAKGLFHKAIMESGVAIIPYLEAHDYEK--SEDLQVVAHFCGNNASDSEALLRCLRTKP 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HCLYLNIYTPADLTKKNRLPVMVWIHGGGLMVGAASTYDGLALAAHENVVVVTIQYRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLAKNLFHRAISESGVALTSVLVKKGDVKPLAEQIAITA---GCKTTTSAAMVHCLRQKT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IWGFFSTGDEHSRGNWGHLDQVAALRWVQDNIASFGGNPGSVTIFGESAGGESVSVLVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IFGFFTTWDQHAPGNWAFKDQVAALSWVQKNIEFFGGDPSSVTIFGESAGAISVSSLILS 244
                                                                                       9669 A Main Street, P.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64; Mismatches 150;
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                                                                                                                                                                    Mutagenesis of Esterases
                                                                                         Box 2509
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RESULT 15
US-08-46-100-30
; Sequence 30, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Millard, Charles B
; APPLICANT: Millard, Charles B
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Best Local Similarity 44.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703) 425-2767 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: broo
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-4250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: p
HYPOTHETICAL: YES
ANTI-SENSE: YES
FRAGMENT TYPE: N
ORIGINAL SOURCE:
ORGANISM: huma:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 EDCLYLNIYAPAHADTGSKLPVLVWFPGGAFKTGSASIFDGSALAAYEDVLVVVVQYRLG 184
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                                                                                                                                                                           GYLQIGANTQAAQKLKDKEVAFWTN 436
                                                                                                                                                                                                             QYLQLDLNMSLGQRLKEPRVDFWTS 547
                                                                                                                                                                                                                                                    ELFSVFGAPFLK-----EGASEEIRLSKMVMKFWANFARNGNPNGKGLPHWPEYNQKE
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                                                                                                                                                                                                                                                                                        EVRFVFGGAFLKGDIVMFEGATEEEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTE 522
                                                                                                                                                                                                                                                                                                                            VKKKOLILDLIADVMFGVPSVIVARNHRDAGAPTYMYEFQYRPSFSSDMKPKTVIGDHGD
                                                                                                                                                                                                                                                                                                                                                                                                       NKQEFGWLIPMQLMSYPLSEGQLDQKTAMSLLGSPIPLFAIAKELIPEATEKYLGGTDDT 297
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US-08-446-100-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 30
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: human esterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Hendricke, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: broomfield
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: FORM: PC-DOS/MS-DOS

SOFTMARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION WIMBER: US/08/446,100

FILING DATE: 19-MAY-1995

CLASSIFICATION: 435

CLASSIFICATION: 435
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TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
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CITY: Fairfax
STATE: VA
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ZIP: 22031
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STREET: 9669 A Main Street, P.O. Box 2509
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                                                                                                                                                                                                                                                                                                                                                                                                303 SKELLTLSQK------TKSFTRVVDGAFFPNEPLDLLSQKAFKAIPSIIGV 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ELFSVFGAPFLK-----EGASEEEIRLSKWVWKFWANFARNGNPNGKGLPHWPEYNQKE 411
                                                                                             EVRFVFGGAFLKGDIVMFEGATEEEKLLSRKWKYWATFARTGNPNGNDLSLWPAYNLTE 522
                                                                                                                                                                                                                                                                                                                                                  EEELLETTLKIGNSYLWTYRETQRHSTLLGTVIDGMLLLKTPEELQRERNFHTVPYMVGI 237
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Search completed: June 15, 2005, 09:43:54 Job time : 30 secs



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Result
No.
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Maximum
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-MODEL=frame+ p2n.model -DEV=xlh
-Q=(cgn2 1)(USPTO_spool)664091/runat_14062005_133640_10461/app_query.fasta_1.775
-DB=GenEmb1 -QFWT=fastap -SUFFIX=p2n.ge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=6664091 @CGN 1 1 4198 @runat 14062005 133640 10461 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DEPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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DB seq length: 2000000000
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100.0
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Match Length DB
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Copyright (c) 1993 - 2005 Compugen Ltd.
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RESULT 1

Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match: DB:	SOURCE SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL PEATURES SOURCE ORIGIN	AR438765 LOCUS DEFINITION ACCESSION VERSION
larity: Similarity:	Unknown. Unknown. Unclassified. Unclassified. 1 (bases 1 to 1746) Curtis,R.A.J. and Si 53010, a human carbo Patent: US 6664091. Location/Q. 11746 /organism=' /mol_type='	AR438765 Sequence 3 from patent AR438765 AR438765.1 GI:42663740
3.08e-252 3079.00 100.00\$ 100.00\$ 100.00\$	Unknown. Unknown: Unclassified. 1 (bases 1 to 1746) 1 (bases 1 to 1746) 53010, a human carboxylesterase family member and uses thereof patent: US 6664091-A 3 16-DEC-2003; Location/Qualifiers 1. 1746 /organism="unknown" /mol_type="genomic DNA"	ď
Length: Matches: Conservative: Mismatches: Indels: Gaps:	antiago,I. Cerase family -DEC-2003; ers ers	1746 bp DNA 75 6664091.
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                                   Patent: WO 0250256-A 3 27-JU
Millennium Pharmaceuticals,
Location/Qualifiers
                                                       Curtis,R.A. and Silos-Santiago,I. 53010, a novel human carboxylesterase thereof
                                                                             Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 3 from Patent W00250256.
AX600126 AX600126.1 GI:28400192
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                                                27-JUN-2002;
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/db_xref="g1:28400191"
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SIFDGSALAXEDVLVVVQVRLGIFGFFTTWDQHAPGWMAFKDQVAALSWVQKNIEF
FGGDPSS'TIFGBSAGAISVSSLILSPMAKGLFHKAIMESGVAIIPYLEAHDYEKSED
LQVVAHFCGNNASDSEALLRCLATKPSKELLTLSQKTKSFTRVYGFXEFPHPQLLLS
QKAFKAIPSIIGVNHECGFLLPMKEAPEILGSKSNKSLALHLIQNILHIPPQYLLLVA
NEYFDDKHSLTEIRDSLLDLLGDVFFVVFALITARYHBDAGAPVYFYERFHRPQCFED
NEYFDKHSLTEIRDSLLDLLGDVFFVVFALITARYHBDAGAPVYFYERFHRPQCFED
TKPAFVKADHADEVRFVFGGAFLKGDIVMFEGATEEBKLLSRKWKYWATFARTGNPN
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/mol_type="unassigned DN/
/db_xref="taxon:9606"
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                                                               PheAlaArgThrGlyAsnProAsnGlyAsnAspLeuSerLeuTrpProAlaTyrAsnLeu
                                                                                               GAAGGAGCCACGGAGGAGGAAGTTACTGAGCCGGAAGATGATGAAATACTGGGCTACC
                                                                                                            GluGlyAlaThrGluGluGluLysLeuLeuSerArgLysMetMetLysTyrTrpAlaThr
                                                                                                                                          GCTGATGAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATGTTC
                                                                                                                                                    AlaAspGluValArgPheValPheGlyGlyAlaPheLeuLySGlyAspIleValMetPhe
                                                                                                                                                                                    TTTCGGCACCGGCCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCAC
                                                                                                                                                                                              PheArgHisArgProGlnCysPheGluAspThrLysProAlaPheValLysAlaAspHis 460
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CE 1 (bases 1 to 2047)

RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altechul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsiah, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Lu, X., Gibbs, R.A., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Rodrigues, S., Bouffard, G.G., Blakesley, R.M., Touchman, J.M., Green, E.D., Bouffard, G.G., Blakesley, R.M., Touchman, J.M., Green, E.D., Bouffard, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
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Clone distribution: MCC clone distribution information can be for
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IBBR Plate: 4 Row: e Column: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
cDNA Library Preparation: Baylor Human Genome Sequencing Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Contact: amg@bcm.tmc.edu
Cunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., 1
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (29-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                           Center code: BCM-HGSC
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Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Director MGC Project.
Direct Submission
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HOmo sapiens hypothetical protein FLJ31547, mRNA (cDNA clone
MGC:97182 IMAGE:7262427), complete cds.
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/tissue_type="PCR rescued clones"
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SerLeuGlyGlnArgLeuLysGluProArgValAspPheTrpThrSerThrIleProLeu
                                                     LeuSerLeuTrpProAlaTyrAsnLeuThrGluGlnTyrLeuGlnLeuAspLeuAsnMet
                                                                                                                                                                             TTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGAAGTTACTGAGC
                                                                                                                                                                                                PheLeuLysGlyAspIleValMetPheGluGlyAlaThrGluGluGluLysLeuLeuSer
                                                                                                                                                                                                                                               AAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTTCGGTGGTGCC
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                                                                                                        CGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACCGGGAATCCTAATGGGAACGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23 from Patent AX477711 AX477711.1 GI:22216866
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Mammalia; Eutheria;
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                                                                                   GlnHisMetLeuLysValHisTyrProLysPheGlyValSerGluAspCysLeuTyrLeu
                                                                                                                                   ArgGluAlaThrSerTyrProAsnLeuCysLeuGlnAsnSerGluTrpLeuLeuLeuAsp
                                                                                                                                                                                 ProProLeuGlySerLeuArgPheThrAsnProGlnProAlaSerProTrpAspAsnLeu
                                                                                                                                                                                                                  GTCACTGTGCTGGGAAGCCCTGTGCTGTGAACGTGTTCCTCGGAGTCCCCTTTGCTGCT
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                                                                                                                      CGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGAT
                                                                                                                                                                     CCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"

mol_type="unassigned DNA"

db_xref="taxon:9606"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                       SerArgLysMetMetLysTyrTrpAlaThrPheAlaArgThrGlyAsnProAsnGlyAsn 510
                                                                                            GCCTTCCTGAAGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGAGAAGTTACTG
                                                                                                            AlaPheLeuLy8GlyAspIleValMetPheGluGlyAlaThrGluGluGluLy8LeuLeu
                                                                                                                                                                                                                                                         AspLeuLeuGlyAspValPhePheValValProAlaLeuIleThrAlaArgTyrHisArg
                                                                                                                                                                   ThrLysProAlaPheValLysAlaAspHisAlaAspGluValArgPheValPheGlyGly
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                                                                                                                                                  ACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTTCGGTGGT
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AUTHORS
TITLE
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VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: ang@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Baylor College of Medicine Human
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Strausberg,R.

Direct Submission

Submitted (01-NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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/mol type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:5174937"
/tissue_type="Brain, Lung, T
/clone_tib="NIH MGC_115"
/lab_host="DH10B"
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Yamamoco,J.1., Isono,Y., H10,Y., Otsuka,K., Nagal,K., Irie,K., Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and Masuho,Y. Pull-length cDNA sequences Patlent: EP 1308459-A 249 07-MAY-2003; Patent: EP 1308459-A 249 07-MAY-2003; Helix Research Institute (JP); Research Association for			AX746724 2092 bp mRNA linear PAT 20-JUN- Sequence 249 from Patent EP1308459.	370 Seriedienginfromhernernernergenderno 361 			1672 AACGACCTGTCTCTGTGGCCAGCTTATAATCTGACTGAGCAGTACCTGCAGCTGGA 530 AsnMetSerLeuGlyGlnArgLeuLysGluProArgValAspPheTrpThrSerTh	1612 CTGAGCCGGAAGATGATGAAAATACTGGGCTACCTTTGCTCGAACCGGGAATCCTAATGGG 510 ABDABDLeuSerLeuTrpProAlaTyrAsDLeuThrGluGlnTyrLeuGlnLeuAspLeu	1552 GGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGAGGAAGTTA 490 LeuserargLysmetmetLysTyrTrpalaThrPhealaArgThrGlyAsnProAsnGly						2 6 6	5 23 6	1072 AGCCAGAAAACAAAGTCTTTCACTCGAGTGGTTGATGGTGCTTTCTTT

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            pAlaPheLysAspGlnValAlaAlaLeuSerTrpValGlnLysAsnIleGluPhePheGl
    TGCACATTTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCTGCTGAGGTGCCTGAGGAC
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Homo sapiens cDNA FLJ33678 fis, clone BRAWH2002191, wee to FATTY ACYL-COA HYDROLASE PRECURSOR, MEDIUM CHAIN (EX AKO90997

AKO90997.1 GI:21749268
oligo capping; fis (full insert sequence).

Homo sapiens (human)

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 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                    PRI 30-JAN-2004 weakly similar (EC 3.1.2.14).
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SI Isogai, T. and Yamamoto, J.

Direct Submission

Submitted (04-7UL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

KAZUSBA-KAMBATATI, Kisarazu, Chiba 292-0812, Japan

(Remail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'-& 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.

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     lAlaHisPheCysGlyAsnAsnAlaSerAspSerGluAlaLeuLeuArgCysLeuArgTh 300
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Percent Similarity: Best Local Similarity: US-10-023-515-2 (1-581) x AK090997 (1-2092) 126 CACTTTAACTGG------GGGCCTTCTGCTGAAGGGCCACAGAGGAACACCAGGCTG 24 HisArgGlnTrpGlyLysThrGlyProSerAlaGluGlyProGlnArgAsnThrArgLeu 43 GlyTrpIleGlnGlyLysGlnValThrValLeuGlySerProValProValAsnValPhe 63 LeuGlyValProPheAlaAlaProProLeuGlySerLeuArgPheThrAsnProGlnPro 83 GGATGGATTCAGGGCAAGCAAGTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTC pAlaPheLysAspGlnValAlaAlaLeuSerTrpValGlnLysAsnIleGluPhePheGl aSerIlePheAspGlySerAlaLeuAlaAlaTyrGluAspValLeuValValValValGl AlaSerProTrpAspAsnLeuArgGluAlaThrSerTyrProAsnLeu------Cy 100 |AlaIleIleProTyrLeuGluAlaHisAspTyrGluLysSerGluAspLeuGlnValVa 280 rLeuIleLeuSerProMetAlaLysGlyLeuPheHisLysAlaIleMetGluSerGlyVa yGlyAspProSerSerValThrIlePheGlyGluSerAlaGlyAlaIleSerValSerSe 240 GTACCGGCTAGGAATATTTGGTTT nTyrArgLeuGlyIlePheGlyPhePheThrThrTpAspGlnHisAlaProGlyAsnTr rGlySerLysLeuProValLeuValTrpPheProGlyGlyAlaPheLysThrGlySerAl 160 ATTCGGAGTGTCAGAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCCACGCCGATAC sPheGlyValSerGluAspCysLeuTyrLeuAsnIleTyrAlaProAlaHisAlaAspTh 140 sLeuGlnAsnSerGluTrpLeuLeuLeuAspGlnHisMetLeuLysValHisTyrProLy 120 GCATCGCCCTGGGATAACTTGCGAGAAGCCACCTCCTACCCTAATTTGTAAGACCAGGTG CTCGGAGTCCCCTTTGCTGCTCCCCCCGCTGGGATCCCCTGCGATTTACGAACCCGCAGCCT TGGGGACCCCAGCTCTGTGACCATCTTTGGCGAGTCCGCGGGAGCCATAAGTGTTTCTAG **ĊTCCATCTTTGATGGGTCCGCCCTGGCTGCCTATGAGGACGTGCTGGTTGTGGTCGTCCA** 6.16e-235 2877.00 98.40% 98.04% 93.44% CTTCACCACATGGGATCAGCATGCTCCGGGGAACTG Length: Matches: Conservative: Mismatches: Indels:

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KEYWORDS
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                                               BC069548 1896 bp mRNA linear PRI
Homo sapiens hypothetical protein FL/31547, mRNA (cDNA
MGC:97193 IMAGE:7262439), complete cds.
BC069548 BC069548.1 GI:46854430
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                                                                                                                                                                                                                                                                                                                                         UThrGluGlnTyrLeuGlnLeuAspLeuAsnMetSerLeuGlyGlnArgLeuLysGluPr
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AUTHORS
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McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, A.N., Gibbs, R.A.
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Baylor Human Genome Sequ
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Submitted (29-APR-2004) National Institutes of Health, Mammalian Sene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Primates;
1 (bases 1 to 1896)
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	72 GluLygSerGluAspLeuGlnValValAlaHigPheCygGlyAsnAsnAlaSerAspSer 291 	Qу 2. рь 9.
	52 HisLyshlaIleMetGluSerGlyValAlaIleIleProTyrLeuGluAlaHisAspTyr 271 	D Q 2
	32 SeralaGlyalaIleSerValSerSerLeuIleLeuSerProMetAlaLysGlyLeuPhe 251 	Qy 23 Db 79
	112 ValGlnLysAsnIleGluPhePheGlyGlyAspProSerSerValThrIlePheGlyGlu 231 	Qy 21 Db 73
	92 TrpAspGlnHisAlaProGlyAsnTrpAlaPheLysAspGlnValAlaAlaLeuSerTrp 211 	Qy 19 Db 67
	72 GluAspValLeuValValValGlnTyrArgLeuGlyIlePheGlyPhePheThrThr 191 	Oy 17
· · · · · · · · · · · · · · · · · · ·	52 GlyGlyAlaPheLy8ThrGlySerAlaSerIlePheAspGlySerAlaLeuAlaAlaTyr 171 	Qy 1:
	32 IleTyrAlaProAlaHisAlaAspThrGlySerLysLeuProValLeuValTrpPhePro 151 .	Qy 13 Db 49
	112 HisMetLeuLysValHisTyrProLysPheGlyValSerGluAspCysLeuTyrLeuAsn 131 	Оу 1: Db 4:
	92 GluAlaThrSerTyrProAsnLeuCysLeuGlnAsnSerGluTrpLeuLeuLeuAspGln 111 	Qy 9 Db 37
	72 ProLeuGlySerLeuArgPheThrAsnProGlnProAlaSerProTrpAspAsnLeuArg 91	О У 3:
	52 ThrValLeuGlySerProValProValAsnValPheLeuGlyValProPheAlaAlaPro 71 	Qу рь 21
	32 ProSerAlaGluGlyProGlnArgAsnThrArgLeuGlyTrpIleGlnGlyLysGlnVal 51 	Оу 3 Db 19
	12 TrpCysPhePheLeuIleLeuGlnProLeuLeuGlyHisArgGlnTrpGlyLysThrGly 31	Qy 1
	15-2 (1-581) x BC069548 (1-1896)	US-10-023-5
	COYES: 6.35e-212 Length: 1896 2606.00 Matches: 503 illarity: 88.77% Conservative: 3 Similarity: 88.25% Mismatches: 6 84.64% Indels: 58 9 Gaps: 2	Alignment Scores Pred. No.: Score: Percent Similari Best Local Simil Query Match: DB:
	KHSLTBIRDSLLDLLGDVFFVVPALITARYHREGATBBEKLLSRKMKYWATFARTGN PNGNDLSLWPAYNLTBQYLQLDLNMSLGQRLKEPRVDFWTSTIPLILSASDMLHSPLS SLTFLSLLQPFFFFCAP"	ORIGIN

REFERENCE

Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

ACCESSION VERSION VERSION KEYMORDS SOURCE ORGANISM	RESULT 11 AX714052 LOCUS	ם אמ	Ş	Db 1	ঠ	Db 1	ð	Db 1	Ś	Db 1	S	Db 1		Db 1	Ś	Db 1	γQ	Db 1	S	Db 1		P &	. 55		Db 1	á	ם מם	Đ	Db &	Q
AX714052.1 GI:29888980 AX714052.1 GI:29888980 Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Cra	AX714052	65 CTCCAGCCTTTCTTTTTCTTTTGTGCTCCT 1	572 LeuGlnProPhePhePhePheCysAlaPro 581	급=	LeuSerAlaSerAspMetLeuHisSerProLeuSerSerLeuThrPh	545 AGCCTCGGACAGAGACTCAAAGAACCGCGGGTGGATTTTTGGACCAGCACCATCCCCCTG 1604	rLeuGlyGlnArgLeuLysGluProArgValAspPheTrpThrSerThrIlePr	485 CTGTCTGTGGCCAGCTTATAATCTGACTGAGCAGTACCTCCAGCTGGACTTGAACATG 1544	512 LeuSerLeuTrpProAlaTyrAsnLeuThrGluGlnTyrLeuGlnLeuAspLeuAsnMet 531	.425 CGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACCGGGAATCCTAATGGGAACGAC 1484	2	2	72 PheLeuLysGlyAspIleValMetPheGluGlyAlaThrGluGluLysLeuLeuSer 49		452 LysProAlaPheValLysAlaAspHisAlaAspGluValArgPheValPheGlyGlyAla 471	391 1391	432 AlaGlyAlaProValTyrFheTyrGluPheArgHisArgProGlnCysPheGluAspThr 451		2 L	5 GCTAATGAATACTTCCATGACAAGCACTCCCTGACTGAAATCCGAGACACGTCTTCTGGAC 1	2 AlaAsnGluTvrPheHisAspLvsHisSerLeuThrGluIleArgAspSerLeuLeuAsp 4	372 Leualaleuhisleui leelmasilleleuhisleerooliniytleuhisleeuval 391 	55 TGTGGCTTCCTGCTGCCTATGAAGGAGGCTCCTGAGATCCTCAGTGGCTCCAACAAGTCC 12	52 CysGlyPheLeuLeuProMetLysGluAlaProGluIleLeuSerGlySerAsnLysSer 3	.095 CTATTGTCTCAGAAAGCATTTAAAGCAATTCCTTCCATCATCATCAGAGTCAATAACCACGAG 1154	rileileGlyValAsnAsnHi	.035 AAAACAAAGTCTTTCACTCGAGTGGTTGATGATCTTTTCCTTAATGAGCCTCTAGAT 1094	312 LysThrLysSerPheThrArgValValAspGlyAlaPhePheProAsnGluProLeuAsp 331	75 GAGGCCCTGCTGAGGTGCCTGAGGACAAAACCCTCCAAGGAGCTGCTGACCCTCAGCCAG 1	292 GluAlaLeuLeuArgCysLeuArgThrLysProSerLysGluLeuLeuThrLeuSerGln 311

` B &	B 8	Dy Qy	B &	P 9	B 8	B &	g 99	B 8	B &	B 8	B 8	DB:	Pred. No.: Score: Percent Simi Best Local S	ORIGIN Alignment	source	TITLE JOURNAL	AUTHORS
232 SerAlaGlyAlaIleSerValSerSerLeuIleLeuSerProMetAlaLy8GlyLeuPhe 251 	GlyGlu 23 	192 TrpAspGlnHisAlaProGlyAsnTrpAlaPheLysAspGlnValAlaAlaLeuSerTrp 211	172 GluAspValleuValValValGlnTyrArgLeuGlyIlePheGlyPhePheThrThr 191	152 GlyGlyAlaPheLyeThrGlySerAlaSerIlePheAgpGlySerAlaLeuAlaAlaTyr 171 	132 IleTyrAlaProAlaHisAlaAspThrGlySerLysLeuProValLeuValTrpPhePro 151	112 HisMetLeuLysValHisTyrProLysPheGlyValSerGluAspCysLeuTyrLeuAsn 131	92 GluAlaThrSerTyrProAsnLeuCysLeuGlnAsnSerGluTrpLeuLeuLeuAspGln 111 	72 ProLeuGlySerLeuArgPheThrAsnProGlnProAlaSerProTrpAspAsnLeuArg 91 	52 ThrValLeuGlySerProValProValAsnValPheLeuGlyValProPheAlaAlaPro 71 	32 ProSerAlaGluGlyProGlnArgAsnThrArgLeuGlyTrpIleGlnGlyLysGlnVal 51 	12 TrpCysPhePheLeuIleLeuGlnProLeuLeuGlyHisArgGlnTrpGlyLysThrGly 31	5-2 (1-581) x AX714052 (1-1962)	. No.: 6.64e-212 Length: 1962 e: 2606.00 Matches: 503 ent Similarity: 88.77% Conservative: 3 Local Similarity: 88.25% Mismatches: 6	Scores:		Full-length cDNAs Patent: EP 1293569-A 736 1 Helix Research Institute (Biotechnology (JP)	
RESULT 12 AK056109 LOCUS DEFINITION	Qy db	g &	g Q	B 8	B &	υb	р . Q	B 8	S & &	Db Q	D Q	සි රි	B &	g Q	g 99	Qу	Qy
12 9 AK056109 1962 bp mRNA linear PRI 30-JAN-2004 ION Homo sapiens cDNA FLJ31547 fis, clone NT2RI2001010, weakly similar to FATTY ACYL-COA HYDROLASE PRECURSOR, MEDIUM CHAIN (BC 3.1.2.14).	572 LeuGlnProPhePhePhePheCysAlaPro 581	552 IleLeuSerAlaSerAspMetLeuHisSerProLeuSerSerLeuThrPheLeuSerLeu 571 	532 SerLeuGlyGlnArgLeuLygGluProArgValAspPheTrpThrSerThrIleProLeu 551 	512 LeuSerLeuTrpProAlaTyrAsnLeuThrGluGlnTyrLeuGlnLeuAspLeuAsnMet 531	492 ArglysMetMetLysTyrTrpAlaThrPheAlaArgThrGlyAsnProAsnGlyAsnAsp 511 	472 PheLeuLysGlyAspIleValMetPheGluGlyAlaThrGluGluGluLysLeuLeuSer 491 	452 LysProAlaPheValLysAlaAspHisAlaAspGluValArgPheValPheGlyGlyAla 471	ALBGIYALBFTOVBITYFFNETYFGLUPNEAFGHIBAFGFFOGLNCYS 1			72 45	352 CysGlyPheLeuLeuProMetLysGluAlaProGluIleLeuSerGlySerAsnLysSer 371		312 LysThrLysSerPheThrArgValValAspGlyAlaPhePheProAsnGluProLeuAsp 331		272 GluLysSerGluAspLeuGlnValValAlaHisPheCysGlyAsnAsnAlaSerAspSer 291 	252 HisLysalaIleMetGluSerGlyValAlaIleIleDroTyrLeuGluAlaHisAspTyr 271

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Salto, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Yamamoto, J., Salto, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokol, T., Furuya, T., Kikawa, R., Omura, Y., Abe, K., Kamihara, K., Kateuta, N., Sato, K., Kikawa, R., Omura, Y., Abe, K., Kamihara, K., Kateuta, N., Sato, K., Kikawa, R., Dujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takipuchi, S., Watanabe, S., Yoshida, Y., Ishida, S., Yokol, T., Yakahashi, Pujii, A., Hara, H., Tanase, T., Nomura, Y., Kanchori, K., Takahashi, Pujii, A., Hara, H., Tanase, T., Nomura, Y., Takiguchi, S., Watanabe, S., Yoshikawa, Y., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Arita, M., Ishigaki, H., Satoh, N., Takami, S., Moriya, S., Moniyama, H., Satoh, N., Takami, S., Toshikawa, Y., Matsunawa, H., Kohihara, T., Sugiyama, A., Takemoto, M., Makapawa, S., Senoh, A., Mizoguchi, H., Suzuki, O., Nakegawa, S., Senoh, A., Mizoguchi, H., Vatanabe, K., Kumagai, A., Itakura, S., Pukuzumi, Y., Fujimori, Y., Komiyama, M., Tashira, M., Tulawa, M., Ohmori, Y., Kawabata, A., Hiliji, T., Kobatake, N., Inagaki, H., Matanabe, K., Sunbata, A., Hiliji, T., Kobatake, N., Nakajima, Y., Mizuo, T., Matamata, T., Matamabe, K., Nakajima, Y., Takahashi, Y., Sasaki, M., Togashi, T., Kobatake, N., Nakajima, Y., Satoh, H., Togashi, T., Sundai, H., Kawabami, S., Sano, S., Okitani, R., Kawabami, T., Nakamira, Y., Takahashi, Y., Nasahita, R., Yamashita, R., Yamashi
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AK056109.1
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Direct Submission
Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
Submitted (24-OCT-2001) Takao Isogai, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (RRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: RAB and
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Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,B., Omura,Y., Abe,K.
Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
NEDO human CDNA sequencing project
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/mol_type="mRNA"
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/clone="NT2RI2001010"
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                                                                     TrpAspGlnHisAlaProGlyAsnTrpAlaPheLysAspGlnValAlaAlaLeuSerTrp 211
                                                                                                                                                                                           GluAspValLeuValValValValGlnTyrArgLeuGlyIlePheGlyPhePheThrThr 191
                                                                                                                                                                                                                                                                                GGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                   ATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTCCCA
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US-10-023-515-2 (1-581) x AK056109
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SVTIFGESAGAISVSSLILSWAKGLIFHKAIMESGYAIIFYLBAHDYEKSEDLQVVAH

FCGNNA5DSEALLRCLRTKPBKELLTLSQKTKSFTRVVDGAFFPNEPLDLLSQKAFKA

IPSIIGVNNHECGFLLPMKEAPEILSGSNKSLALHLIONIHHIPQXLHIVANBYFHD

KHSLTEIRDSLLDLLGDVFFVVPALITARYHREGATEEEKLLSRKWMKYWATFARTGN

PNGNDLSLWPAYNLTEGYYLQLDLNMSLGQRIKBPRVDFWTSTIFLILSASDMLHSPLS

SLTFLSLLQPFFFFCAP"
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/clone lib="M72RI2"
/note="cloning vector: pME18SFL3-mRNA from NT2 neuronal
precursor cells treated 2-weeks mitotic inhibitor after
5-weeks retinoic acid (RA) induction.-majorly NT2 neuron"
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Oy 191 ThrTrphapGlnHishlaProGlyAsnTrphlaPheLysAspGlnVallaAlaLlaLeuSer 210	171 TyrGl 694 TATGA	Qy 151 ProGlyGlyAlaPheLysThrGlySerAlaSerTlePheAspGlySerAlaLeuAlaAla 170	Qy 131 AsnIleTyrAlaProAlaHisAlaAspThrGlySerLysLeuProValLeuValTrpPhe 150	Oy 111 G1nHisMetLeuLysValHisTyrProLysPheGlyValSerGluAspCysLeuTyrLeu 130	Qy 91 ArgGluAlaThrSerTyrProAsnLeuCysLeuGlnAsnSerGluTrpLeuLeuLeuAsp 110	Qy 71 ProProLeuGlySerLeuArgPheThrAsnProGlnProAlaSerProTrpAspAsnLeu 90	Qy 51 ValThrValLeuGlySerProValProValAsnValPheLeuGlyValProPheAlaAla 70	Qy 31 GlyProSexAlaGluGlyProGlnArgAenThrArgLeuGlyTrpIleGlnGlyLy8Gln 50	6 Gaps: 581) x AX958392 (1-1857)	Fred. No.: 1.91e-210 Length: 1857 Score: 2588.50 Matches: 491 Percent Similarity: 94.62% Conservative: 1 Best Local Similarity: 94.42% Mismatches: 5 Query Match: 84.07% Indels: 23	ORIGIN Alignment Scores:		Human dru Patent: W Incyte Ge	±.4.€		AESULT 13 AX958392 AX958392 LOCUS AX958392 DEFINITION Sequence 20 from Patent WO0226988.	Db 1695 CTCCAGCCTTCTTTTCTTTTGTGCTCCT 1724

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                                                                                                         AspLeuSerLeuTrpProAlaTyrAsnLeuThrGluGlnTyrLeuGlnLeuAspLeuAsn
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Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                      ValThrValLeuGlySerProValProValAsnValPheLeuGlyValProPheAlaAla
                                                                                                                                                                                                                                                                                                                                                                         GluSerhlaGlyAlaIleSerValSerSerLeuIleLeuSerProMetAlaLySGlyLeu
                                                     TrpValGlnLysAsnIleGluPhePheGlyGlyAspProSerSerValThrIlePheGly
                                                                               ThrTrpAspGlnHisAlaProGlyAsnTrpAlaPheLysAspGlnValAlaAlaLeuSer
                                                                                                                              TyrGluAspValLeuValValValValGlnTyrArgLeuGlyIlePheGlyPheFheThr
                                                                                                                                                     AACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTTGCTT
                                                                                                                                                                                                    AsnIleTyrAlaProAlaHisAlaAspThrGlySerLysLeuProValLeuValTrpPhe
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/mol_type="unassigned DNJ/db_xref="taxon:9606"
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                   Canis familiaris (dog)
Canis familiaris
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ProGlyGlyAlaPheLysThrGlySerAlaSerIlePheAspGlySerAlaLeuAlaAla 170
                                                                                  AsnIleTyrAlaProAlaHisAlaAspThrGlySerLysLeuProValLeuValTrpPhe
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KADHSDEIRFVFGGAFLKGNIVMFEGATEEBKLLSRKMRTVYANUFATGDEPNGEGLFY
WPAYSQSEQYLKLDLNISVGQKLKEQEVEFWSDTLPLIMSMSTAPPGPPVPLLSLSVL
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510 1512	491 SerargLysMetMetLysTyrTrpAlaThrPheAlaArgThrGlyAsnProAsnGlyAsn
490 1452	471 AlaPheLeuLysGlyAspIleValMetPheGluGlyAlaThrGluGluGluLysLeuLeu
470 1392	451 ThrLysProAlaPheValLysAlaAspHisAlaAspGluValArgPheValPheGlyGly
450 1332	
430 1272	411 AspLeuLeuGlyAspValPhePheValValProAlaLeuIleThrAlaArgTyrHisArg
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390 1152	371 SerLeuAlaLeuHisLeuIleGlnAsnIleLeuHisIleProProGlnTyrLeuHisLeu
370 1092	351 GluCysGlyPheLeuLeuProMetLysGluAlaProGluIleLeuSerGlySerAsnLys
350 1032	331 AspLeuLeuSerGlnLysAlaPheLysAlaIleProSerIleIleGlyValAsnAsnHis
330 972	311 GlnLysThrLysSerPheThrArgValValAspGlyAlaPhePheProAsnGluProLeu :::
310 912	291 SerGluAlaLeuLeuArgCygLeuArgThrLygProSerLygGluLeuLeuThrLeuSer
290 852	271 TyrGluLysSerGluAspLeuGlnValValAlaHisPheCysGlyAsnAsnAlaSerAsp
270 792	251 PheHistysAlaIleMetGluSerGlyValAlaIleIleProTyrLeuGluAlaHisAsp
250 732	231 GluSerAlaGlyAlaIleSerValSerSerLeuIleLeuSerProMetAlaLy8GlyLeu
230 672	211 TrpValGlnLy8AsmIleGluPhePheGlyGlyAspProSerSerValThrIlePheGly
210 612	191 ThrTrpAspGlnHisAlaBroGlyAsnTrpAlaPheLysAspGlnValAlaAlaLeuSer
190 552	171 TyrGluAspValLeuValValValGlnTyrArgLeuGlyIlePheGlyPhePheThr
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1693 GIGCICCTGCCTTATICTCCTCTGCTCCT 1725	693 GTGC	pb 1
571 LeuLeuGlnProPhePhePhePheCysAlaPro 581	571 LeuL	Ą
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1573 ATAAGCGTGGGACAGAAACTGAAGGAGCAGGAGGTGGAGTTTTGGTCAGATACTCTCCCC 1632	573 ATAA	Db 1
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ALIGNMENTS

SOURCE ORGANISM REFERENCE AUTHORS REFERENCE AUTHORS TITLE JOURNAL ACCESSION VERSION KEYWORDS RESULT 1 AK077248 REFERENCE DEFINITION Shoons JOURNAL MEDLINE TITLE AUTHORS MEDLINE PUBMED PUBMED Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muzamatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) AK077248 11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length enriched library, clone:5031415B19 product:similar to CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ALI-ESTERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAINE ESTERASE) (FROCAINE ESTERASE) (METHYLBUTYRASE) [Mesocricetus auratus], full Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., C. Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Genome Res. 20499374 Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999) Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; Mus musculus HTC; CAP trapper. AK077248 AK077248.1 GI:26346111 1042159 0349636 nsert sequence. musculus (house mouse) Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus HTC 03-APR-2004 Murinae; Mus. Carninci, P.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayatsida, K., Hayatsu, N., Hiramoto, K., Hiracka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Ohacka, M., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sagabe, Y., Tagama, M., Tagawa, A., Takahashi, F., Takaku, Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, T., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mailigenome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9218,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Group Phase I & II Team.

Analysis of the mouse transcriptome based of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2687)

6 (bases 1 to 2687)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepare mouse tissues.
Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FANTOM Consortium.

Functional annotation of a full-length

""" 409, 685-690 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The FANTOM Consortium and the RIKEN Genome Exploration Research
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                                                                                                                                        /note="unnamed protein product; putative similar to CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ALI-ESTERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAINE ESTERASE) (METHYLBUTYRASE)
                                                                                            83%ID, 100%length,
                                                                                                                                                                                                                                                              /tissue type="ovary and uterus"
/clone_Tib="RIKEN full-length enriched mouse
/dev_stage="11 days pregnant adult"

                                                                             Wesocricetus auratus) (SPTR | O35533, evidence: FASTY, 100%length, match=1677)"
Codon start-1
translation="MPLYKLLGWLNAVACGVLLLVLHVQGQDSASPIRNTHTGQVRGS"
                                                                                                                                                                                                                                                                                                                                              'sex="female"
                                                                                                                                                                                                                                                                                                                                                                        clone="5031415B19"
                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="FANTOM_DB:5031415B19"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
|mol_type="mRNA"
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                         otein_id="BAC36707.1"
_xref="GI:26346112"
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            CTCTTCCATGGTGCCATCATGGAGAGTGGAGTAGCTGTGCTCCCTGATCTTATCTCCAGC
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LeuPheHisLysAlaIleMetGluSerGlyValAlaIleIleProTyrLeuGluAlaHis
                                                                                                                GlyGluSerAlaGlyAlaIleSerValSerSerLeuIleLeuSerProMetAlaLy8Gly 249
                                                                                                                                                                                                                  SerTrpValGlnLysAsnIleGluPhePheGlyGlyAspProSerSerValThrIlePhe
                                                                                                                                                                                                                                                                                                                                                 ThrThrTrpAspGlnHisAlaProGlyAsnTrpAlaPheLysAspGlnValAlaAlaLeu
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                                                                          GGAGAGTCAGCAGGTGGCACAAGTGTGTCTTCACATGTTGTGTCCCCCATGTCCCCAGGGA
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GSEDLKMMNLILPPISMSEDCLYLNIYVPAHAHEGSNLPVMWHIGGALTVGWASMYD
GSMELKMMVLILPPISMSEDCLYLNIYVPAHAHEGSNLPVMWHIGGALTVGWASMYD
GSMELATEBUVVUVAIOXFLGVLGFFSTGDQHAKGNMGYLDQVIALRWVQQNIVHFGGN
PDRVTIFGESAGGTSVSSHVVSSMSQGLFHGALMESGVAVLFDLISSSSEMVIRIVAN
PDRVTIFGESAGGTSVSSHVVSSMSGGLFHGALMESGVAVLFDLISSSSEMVIRIVAN
LSGCAAVNSETLMCCLAGKNBAEMLALMKVFKIIFGVUDGEFLJKHPDECDLMAE
VPSIIGINNDEXGWILPTIMDPAQKIEEITRKTLPAVLKSTALKMLPPECGDLLMEE
VMGDTEDDETLQAQFREMKGDEMFVIPALGVAHFQRSHAFVVYFYEFQHRESFFKDFRP
PYVKADHGDEIFLVFGYQFGNIKLPYTEEEEQLSRALMKYMANFARHGNENGEGLPYW
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AK033563 2661 bp mRNA linear HTC 03-APR Mus musculus adult male colon cDNA, RIKEN full-length enriched library, clone:9030624L02 product:similar to CARBOXYLESTERASE
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                                                                                                                                                        SerAlaSerAspMetLeuHisSerPro-------
                                                                                                                                                                                                                                 GTGATGGACCATGATGAGCAGTACCTGCAGCTGGACATCCAGCCTTCTGTGGGTCGAGCC
                                                                                                                                                                                                                                                    AlaTyrAsnLeuThrGluGlnTyrLeuGlnLeuAspLeuAsnMetSerLeuGlyGlnArg
                                                                                                                                                                                                                                                                                                    TyrTrpAlaThrPheAlaArgThrGlyAsnProAsnGlyAsnAspLeuSerLeuTrpPro 516
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P. Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiramoto, K., Hiramoto, K., Hiramota, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Parangashi, M., and Hayashizaki, Y.
                                                                                                                                                     Submitted (16-UIL-2001) Yoshihide Hayashizaki, The Institute c Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC RIKEN Yokohama Institute; 1-7-22 Suehiro-Cho, Tsurumi-ku, Yoko Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax.81-45-503-9216)
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CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rigeronic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to
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Analysis of the mouse transcriptome based of 60,770 full-length cDNAs
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/.
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
               LeuAsnIleTyrAlaProAlaHisAlaAspThrGlySerLysLeuProValLeuValTrp
                                                           GATCTGAAGATGATGATCTTGATCCTGCCTCCCATCTCTATGTCTGAGGACTGCCTGTAT
                                                                                 AspGlnHisMetLeuLysValHisTyrProLysPheGlyValSerGluAspCysLeuTyr 129
                                                                                                                                                               ArgGluAlaThrSerTyrProAsnLeuCysLeuGlnAsnSerGluTrpLeu---LeuLeu
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(ALL-ESTERASE) (B-ESTERASE) (MONDHTYRASE) (COCAINE ESTERASE) (MONDHTYRASE)
(PROCAINE ESTERASE) (METHYLBUTYRASE)
(Mesocricetus auratus) (SPTR|03533, evidence: FASTY, /Codon start=1
/protein_id="BAC28361.1"
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This sequence was made by sequencing genothem based on alignment
Location/Qualifiers
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Direct Submission
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Terriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/locus_tag="HCM5231"
                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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                            CCTGTCCCCAGCATCATTGGTTTCAACAATGATGAGTATGGTTGGATCGTCCCCAAAAGC
                                                AlaIleProSerIleIleGlyValAsnAsnHisGluCysGlyPheLeuLeuProMetLys 359
                                                                                                             ValAspGlyAlaPheProAsnGluProLeuAspLeuLeuSerGlnLysAlaPheLys
                                                                                                                                                 GCCAAGAGTGAAGCAGAGATTCTGGCTATTAACAAGAACTTCCAGATGATCCCTGGTGTG
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P. Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
                                                                                                                                                   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new
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Meth. Enzymol.
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Eukaryota; Me
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1958 bp mRNA linear HTC 03-APR-2004 Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130231C15 product:similar to LIVER CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) [Mesocricetus auratus], full insert
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zymol. 303, 19-44 (1999)
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

ALL Nature 420, 563-573 (2002)

B (bases 1 to 1958)

Adachi,J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nasaki, T., Saitoh, H., Sakai, C., Sano, H., Sasaki, D., Shibata, K., Numazaki, R., Ohno, M., Ohsato, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tanaka, T., Tomaru, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M. and Hayashizaki, Y., Toya, T., Yasunishi, A.,
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Submitted (16-ARR-2002) Yoshihide Hayashizaki, The Institute of Submitted (16-ARR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, RIKEN Yokohama, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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Genomic Sciences Center and Genome Science Laboratory in R
Division of Experimental Animal Research in Riken contribu
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Please visit our web site for further details.
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DRVTIFGVSAGGTSVSSHILSBMSKGIPHGAIMQSGVALLPDLISDTSEVVYKYVANI
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KEYWORDS
SOURCE
ORGANISM
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ACCESSION VERSION KEYWORDS	RESULT 5 AY414459 LOCUS DEFINITION	Db	Ş		Ş	뫄	Ş	P. 5		Ş	B 8	дb	Ş		Ś	8 8		S.			문 5			Db	Ş	망	\$	Db
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Submitted (16-NOV-2003) Celera Genomics,
Rockville, MD 20850, USA
This sequence was made by sequencing gene
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(bases 1 to 1680)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous
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Science 302 (5652), 1960-1963 (2003)
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/organism="Homo sapiens"
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                                            LeuThrGluGlnTyrLeuGlnLeuAspLeuAsnMetSerLeuGlyGlnArgLeuLysGlu
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                          CAGGAGGAGCAATACCTGCAGCTGAACCTACAGCCTGCGGTGGGCCCGGGCTCTGAAGGCC
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                                                                                  Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayateu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hirozane, T., Hirozane, T., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komno, H., Kouda, M., Koya, S., Kurihara, C., Mateuyama, T., Myazaki, A., Ohno, M., Ohsato, N., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sagabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramateu, M. and Hayashizaki, Y., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Physical and Chemical Research (RIKEN), Laboratory Exploration Research Group, RIKEN Genomic Sciences
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                     oGlyGlyAlaPheLysThrGlySerAlaSerIlePheAspGlySerAlaLeuAlaAlaTy 171
                                                                                                                                                                                  nHisMetLeuLysValHisTyrProLysPheGlyValSerGluAspCysLeuTyrLeuAs 131
TGGTGGTGGACTGGTTGCAGGCATGGCTTCCATGTATGATGGATCCGTGCTGGCAGCCAC
                                                                             CATCTACACACCAGCCCAGGAGGGCTCTAACCTGCCTGTGATGGTGGCTCCA
                                                                                                                   nIleTyrAlaProAlaHisAlaAspThrGlySerLysLeuProValLeuValTrpPhePr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similar to CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ALI-ESTERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="thymus"
/clone_lib="RIKEN full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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db_xref="taxon:10090"
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                  GAACCCCAACAGTGAGGATCTACCCTACTGGCCAGCGTCAAACCAAGATGATCTGTACCT
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                                                                                                     uGluGluLysLeuLeuSerArgLysMetMetLysTyrTrpAlaThrPheAlaArgThrGl
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Length

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sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp434N0935) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Htp://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp434N0935 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann@dkfz-heidelberg.de;
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
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Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2888 bp. mRNA linear HTC 22-SEP-20 mRNA linear HTC 22-SEP-20 homo sapiens mRNA; cDNA DKFZp434N0935 (from clone DKFZp434N0935).
AL713761
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/tissue type="testis"
/clone_Tib="434 (synonym: h
DH10B; sites NotI + SalI"
/dev_stage="adult"
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FEATURES Location/Qualifiers	http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686H0466 http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686H0466 Further information about the clone and the sequencing project is	This clone (DKFZp686H0466) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.	Bequenced by GBF (National Rebeaton Centre for Elocechnology Erd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.	Neuherberg, GERMANY Clone from S. Wiemann, Molecular Genome Analysis, German Can Research Center (DKFZ); Email s. wiemann@dkfz-heidelberg.de;	Osanger, A., Fobo,G., Han, M. and Wiemann, S. The German CDNA Consortium Direct Submission Submitted (22-SEP-2004) MIPS. Ingolstaedter Landstr.1, D-	Eukaryota; Metazoa; Chordata; Crani Bukaryota; Metazoa; Chordata; Crani Mammalia; Eutheria; Primates; Catar 1 (bases 1 to 3909)		HSM806270 HSM806270 3909 bp mRNA linear HTC 22-SEP-2004 DEFINITION Homo sapiens mRNA; cDNA DKFZp686H0466 (from clone DKFZp686H0466).	:::			TOO FINGS YATE III GLUG AGEAGGA GARGAI SEICHNEUR AND AGEAGGARGAI SEICHNEUR AGEAGGARGAI SEICHNEUR AGEAGGARGAI SEICHNEUR AGEAGGARGAI SEICHNEUR AGEAGCA GARGAI SEICHNEUR AGEAGCA GARGAI SEICHNEUR AGEAGCA GARGAI SEICHNEUR AGEAGCA GARGAI SEICHNEUR AGEAGAI 100 Alexanologia validation (2454 GAGTTCCAGCATCAGCCCAGCTGGCTCAAGAACATCAGGCCACCGCACATGAAGGCCAGC 2454 GAGTTCCAGCATCAGCCCAGCTGGCTCAAGAACATCAGGCCACCGCACATGAAGGCCAGC 2450 WisalaacGluValacadacadacadacadacadacadacadacadacadac	2397	2337 GGGGATCCCCAGACCCTCCAAGCGCAGTTCCAGGAGATGATGGCGGACTCCATGTTTGTG	::: :::	Db 2217 GATACCCAGAAGGAAATGGACAGAGAGAGGCCTCCCAGGCTGCTCCAGAAAATGTTAACG 2276	360	Db 2157 ATTGTTGGTGTCAACAACAATTGAATTCGGCTGATCCCCCAAGGTCATGAAGATCTAT 2216	

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                               LeuThrGluGlnTyrLeuGlnLeuAspLeuAsnMetSerLeuGlyGlnArgLeuLysGlu
                                                                             AACTTTGCGAGAAATGGGAATGGCGAGGGTCTGCCACACTGGCCGCTGTTCGAC
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Alignment Scores: Pred. No.: 1158.50 Score: Score: 1158.50 Matches: 255 Percent Similarity: 44.58* Query Match: 37.63* DB: 1 MetProGlnGlyLeuThrSerSerAlaSerGlnTrpCysPhebLeuIleLeu 18 1::	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 42 Row: p Column: 20 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein This clone has the following problem: frame shifted. FEATURES 1. 2038 1. 2038 1. 2038 1. 2038 1. 2038 1. 2038 1. 2038 1. 2038 1. 2038 2. 2038	NIH-MGC Project URL: http://mgc.nci.nih.gov CONMENT Contact: MGC help desk CONMENT Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.	Qy 540 ProArgValAspPheTrpThrSerThrIlePro 550 ::: Db 2742 CACAGGCTCCAGTTCTGGAAGAAGGCGCTGCCC 2774 RESULT 9 BC019926 BC019926 BC019926 LOCUS BC019926 CONBERION BC019926 BC019926 BC019926 BC019926 BC019926 BC019926 CONBERION BC019926 BC019926 CONBERNOR BC019926 BC019926 CONBERNOR BC019926 BC019926 BC019926 CONBERNOR BC019926 BC019926 CONBERNOR BC019926 BC019926 CONBERNOR BC019926 BC019926 CONBERNOR BC019926 BC019926 CONBERNOR BC019926 BC019926 CONBERNOR BC019926 BC019926 CONBERNOR BC019926 BC019926 CONBERNOR BC019926 CONBERNOR BC019926 BC019926 CONBERNOR BC019926 BC019926 CONBERNOR BC019926 BC019926 CONBERNOR BC019926 CONBERNOR BC019926 BC019926 CONBERNOR BC019926 BC019926 CONBERNOR BC019926 BC019926 CONBERNOR BC019926 CONBERNOR BC019926 BC019926 CONBERNOR BC019926 BC019926 CONBERNOR BC019926 BC019926 CONBERNOR BC019926 BC0199
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
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Meth. Enzymol. 3
99279253
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mus musculus (house
Mus musculus
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Sciurognathi; Muridae; Murinae; Mus
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      LeuIleLeuGlnProLeuLeuGlyHisArgGlnTrpGlyLysThrGlyProSerAlaGlu
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US-10-023-515-2 (1-581) x AK037191 (1-2356)
                                                                                                            Percent Similarity:
Best Local Similarity:
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URL:http://fantom.gsc.riken.jp/.
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Submitted (16-UTL-2001) Yoshihide Hayashizaki, The Institute c
Submitted (16-UTL-2001) Yoshihide Hayashizaki, The Institute c
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yoko
Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P. Pukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiranoka, T., Hirozane, T., Hari, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Konno, H., Kouda, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takhisahi, F., Takaku-Akahira, S., Muramatsu, M., and Hayashizaki, Y., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
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Analysis of the mouse transcriptome of 60,770 full-length CDNAs
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                                                                                                                                                                                                                                                                                                                     protein
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/clone_Iib="RIKEN full-length enriched
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/clone="A030007M20"
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/strain="C57BL/6J"
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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P. Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Haradda,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RS Adachi, J. Aizawa, K. Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayatsun, M., Hiranoto, K., Haraoka, T., Hirozane, T., Hayatsun, M., Hiranoto, K., Haraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Marsuyama, T., Miyazaki, A., Murata, M., Oho, M., Ohsato, N., Okazaki, Y., Saito, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Okazaki, Y., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku, Akahira, S., Takadu, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Toya, T., Yasunishi, A., Muramatsu, M. and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gc.riken.jp, Fax:81-45-503-9212,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prepare mouse tissues.
Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group Genomic Sciences Center and Genome Science Laboratory in R Division of Experimental Animal Research in Riken contribu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1944)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The FANTOM Consortium and the
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/protein_id="bac37439.1"
/dp.ref="G:26347581"
/translation="mglyplirulslaactawgypssppvvntvkgkvuckkyvnlegft
/translation="mglyplirulslaactawgypssppvvntvkgkvuckkyvnlegft
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gesaggfesvsvlvlsplaknlfhraisesgvsltaalittdvkpiaglvatlsgcktt
                                                                                                                                                                                               match=1939)
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                                                                                                                                                                                                                                                                                           /tissue_type="colon"
/clone_lib="RIKEN full-length
                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J"
/db_xref="FANTOM_DB:9030604P03"
/db_xref="taxon:10090"
                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                                                                                                               /clone="9030604P03"
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GlyLeuPheHisLysAlaIleMetGluSerGlyValAlaIleIleProTyrLeuGluAla
                                                                                        PheGlyGluSerAlaGlyAlaIleSerValSerSerLeuIleLeuSerProMetAlaLys 248
                                                                                                                                                         CTACGCTGGGTCCAGGACAACATTGCCAACTTTGGGGGCAACCCAGGCTCGGTGACCATC
                                                                                                                                                                                                   LeuSerTrpValGlnLysAsnIleGluPhePheGlyGlyAspProSerSerValThrIle
                                                                                                                                                                                                                                                                                                 PheThrTrpAspGlnHisAlaProGlyAsnTrpAlaPheLysAspGlnValAlaAla
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LAEKSFSTVPYIVGINKQEFGWIIPTLMGYPLAEKSLLOKTANSLAKSYPTLKISEN
MIPVVAEKYLGGTDLLTKKKDLFQDLMADVVPGVPSVIVSRSHRDAGASTYMYEBEYE
PSFVSAMRPKAVIGDHGDEIFSVFGSPFLKDGASEETNLSKMVMKFWANFARNGNPN
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EST.
Rattus norvegicus (Norway rat)
                                                                                 CF111083

1918 bp mRNA linear EST 23-JUL Shultzomica04334 Rat lung airway and parenchyma cDNA libraries Rattus norvegicus cDNA clone Contig3845 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuSerGlnLysThrLysSerPhe------
                                                                                                                                                                                                                                                                                                                                                                                AspThrLysProAlaPheValLysAlaAspHisAlaAspGluValArgPheValPheGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuAspLeuLeuGlyAspValPhePheValValProAlaLeuIleThrAlaArgTyrHis 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCAATTCTCTCTTGTGGAAGTCCTACCCAACACTTAAAATCTCTGAGAATATGATTCCA 1248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCTTCCTCCCTACTĠĬĠATTĠĂĬĠĠÁGTAGTTCTGĊĊĂAAGGCAĆĊĂGAAGAGATCĊĨĠ
                                                                                                                                                                                                                                                     ProLeuIleLeuSerAlaSerAspMetLeuHisSerPro 562
                                                                                                                                                                                                                                                                                              TCAACTCAGGCAGCCCAGAGGCTGAAGGACAAAGAAGTGAGTTTTTTGGGCTGAG-----
                                                                                                                                                                                                                                                                                                                                   AsnMetSerLeuGlyGlnArgLeuLysGluProArgValAspPheTrpThrSerThrIle
                                                                                                                                                                                                                                                                                                                                                                                                                     AsnAspLeuSerLeuTrpProAlaTyrAsnLeuThrGluGlnTyrLeuGlnLeuAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCAGCAAGATGGTGATGAAATTCTGGGCCAACTTTGCTCGGAATGGGAACCCCCAATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuSerArgLysMetMetLysTyrTrpAlaThrPheAlaArgThrGlyAsnProAsnGly 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyAlaPheLeuLysGlyAspIleValMetPheGluGlyAlaThrGluGluGluLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCATGAGACCCCAAGGCAGTAATAGGAGACCATGGTGATGAGATCTTCTCAGTATTTTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGATCATTCCAACGCTTATGGGCTATCCACTCGCTGAAGGCAAACTGGACCAGAAGACA 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PheLeuLeuProMetLysGluAlaProGluIleLeuSerGlySer---AsnLysSerLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerAspSerGluAlaLeuLeuArgCysLeuArgThrLysProSerLysGluLeuLeuThr 308
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                                                                                                                                                                                                                 CTCAGGGCCAAGGAGTCAGCCCAGAGGCCA 1734
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
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Location/Qualifiers
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1311 Haring Hall, One Shields
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dept. of Molecular Biosciences, School of Veterinary Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Shultz MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing and microarray development Am. J. Respir. Cell Mol. Biol. 30 (3),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mashultz@ucdavis.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
  TyrProLysPheGlyValSerGluAspCysLeuTyrLeuAsnIleTyrAlaProAlaHis 137
                                                                  GTTGGAGGGCAGGTTCTCAGAGAGCTTTTCACCAACAGGAAAGGAAAACATTCCTTTACAG
                                                                                                                                                    GAGTCTTGGAACTTTGTGAAGAATACTACCTCCTACCCACCTATGTGCTCTCAAGATGCT
                                                                                                                                                                                   SerProTrpAspAsnLeuArgGluAlaThrSerTyrProAsnLeuCysLeuGlnAsn---
                                                                                                                                                                                                                                  GGAATCCCCTTCGCCAAGTCCCCTCTTGGCTCCTTGAGGTTTGCTCCACCACAGCCTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ArgGlnTrpGlyLysThrGlyProSerAlaGluGlyProGlnArgAsnThrArgLeuGly 44
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530 752 4698
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/dev stage="adult"
/clome_lib="Rat lung airway and parenchyma cDNA libraries"
/clome_lib="Rat lung; Vector: pGEM-112f(-); Site_l: Eco RI;
/note="Organ: lung; Vector: pGEM-112f(-); Site_l: Eco RI;
Site_2: Not I; mRNA was isolated from microdissected rat
lung_airways and parenchyma tissues."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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                                                                                                       -SerGluTrpLeuLeuAspGlnHisMetLeuLysValHis
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Matches:
Conservative:
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Indels:
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                                                                                                                                                              GGTGTCCCATCAGTGATGGTGTCTCGAAGTCACAGAGATGCTGGAGCCCCCACCTTCATG 1363
                                AspHisAlaAspGluValArgPheValPheGlyGlyAlaPheLeuLysGlyAspIleVal 478
                                                                                                                                                                                        ValValProAlaLeuIleThrAlaArgTyrHisArgAspAlaGlyAlaProValTyrPhe 438
                                                                                                                                                                                                                                               ACAGATGACCCTGCCGAAAGGAAAGACCTGTTCAAGGACTTGGTTGCAGATGTGATATTT 1303
                                                                                                                                                                                                                                                                                                                                                                                                                CCACTCTCCGAAGGCAAACTGGACCAGAAAACAGCCAATTCCCTCTTGTGGAAGTCCTAC 1183
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TACATAGTGGGCATCAACAAGCAAGGATTTGGCTGATCATTCCAATGCTTATGGGCTAT 1123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGGTGCTGTCAAAGACACCAGAAGAGATCCTGGCTGAGAAGAGTTTCAACACGGTCCCC
                                                                          TATGAATTTGAGTATCGCCCAAGCTTTGTATCAGCCATGAGGCCCAAGACAGTGATCGGA 1423
                                                                                                                    TyrGluPheArgHisArgProGlnCysPheGluAspThrLysProAlaPheValLysAla 458
                                                                                                                                                                                                                                                                                                                              CCAACACTGAAAATCTCTGAGAAAATGATTCCAATGGCTTCTGAGAAGTATTTAGGAGGG 1243
GACCATGGTGATGAAATCTTCTCAGTATTTGGATCTCCATTTTTAAAA----
                                                                                                                                                                                                                                                                                  LysHisSerLeuThrGluIleArgAspSerLeuLeuAspLeuLeuGlyAspValPhePhe 418
                                                                                                                                                                                                                                                                                                                                                                        ---IleLeuHisIleProProGlnTyrLeuHisLeuValAlaAsnGluTyrPheHisAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluIleLeuSerGlySer---AsnLysSerLeuAlaLeuHisLeuIleGlnAsn-----
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AUTHORS
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Submitted (20-UUL-2004) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

Web: www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
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1 (Dases 1 to 1826)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation
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                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="CSODE014YC12"
/tissue_type="placenta"
/plasmid="pCMVSPORT_6"
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                                      TyrLeuHisLeuValAlaAsnGluTyrPheHisAspLysHisSerLeuThrGluIleArg
                                                                                                                                     GlySerAsnLysSerLeuAlaLeuHisLeuIleGlnAsnIleLeuHisIleProProGln
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Direct Submission

Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage

Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage

1 zue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

(E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

The sequences are based on single pass reads.

More information available at

http://www.genoscope.cns.fr/tetraodon.

Location/Qualifiers
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Tetraodon nigroviridis full-length cDNA.

CR641368.1 GI:51137813

HTC; cDNA; full-length; Tetraodon nigroviridis.

Tetraodon nigroviridis

Tetraodon nigroviridis

Tetraodon nigroviridis

Tetraodon nigroviridis

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Tetraodon Tetraodontidas; Chaniata; Vertebrata; Euteleostomi;

Acanthomorpha; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontidos; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae
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                     (1-581)
                                                                                                                                                                                                                                                                                               /organism="Tetraodon nigroviridis"
/mol_type="mRNA"
/db_xref="taxon:99883"
                                                                                                                                                                                                                                                                           tissue_type="Liver"
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1055.00
59.70%
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34.26%
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Matches:
Conservative:
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ProPro-----GlnTyrLeuHisLeuValAlaAsnGluTyrPheHisAspLysHis
                                  CACGTCTCTGGT
                                                  IleLeuSerGlySerAsnLysSerLeuAlaLeuHisLeuIleGlnAsnIleLeuHisIle
                                                                                                           GlyPheLeuLeuProMetLysGluAlaPro-----Glu
                                                                                                                                                                 LeuSerGlnLysAlaPheLysAlaIleProSerIleIleGlyValAsnAsnHisGluCys
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                                                                                                                                                                                                                     ThrLysSerPheThrArgValValAspGlyAlaPhePheProAsnGluProLeuAspLeu
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                                                                                 GGTTGGTTÄCTTGCTCGGTACTTTGCTCCTCCAAACTGGACAGAGGGGATGGACCAGGAA
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                                                                                                                                                                                                                                                                                                                                SerGluAspLeuGlnValValAlaHisPheCysGlyAsnAsnAlaSerAspSerGluAla 293
                                                                                                                                                                                                                                                                                                                                                            GCAATTGCTGAAAGTGGCACTGCTGCAATG---CATATATTTGCTCAAGAT---GACCCC 820
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|TAGAAGTCAACCTTCCA-----GACATTTCAGAAGACTGCCTTTACCTCAACATTTAC
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The sequences are based on single pass reads.
More information available at
http://www.genoscope.cns.fr/tetraodon.
Location/Qualifiers
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Tetraodon nigroviridis full-length cDNA.
CR634885
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CR634885.1 dll-length; Tetraodon nigroviridis.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleosteei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidea; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; T
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                                      364 IleLeuSerGlySerAsnLysSerLeuAlaLeuHisLeuIleGlnAsnIleLeuHisIle 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAATTGCTGAAAGTGGCACTGCTGCAATG---CATATATTTGCTCAAGAT---GACCCC 800
                                                                          GTTGGTTACTTGCTCGGTACTTTGCTCCTCCAAACTGGACAGAGGGGATGGACCAGGAA 1100
                                                                                                                  GlyPheLeuLeuProMetLysGluAlaPro------Glu 363
                                                                                                                                                            TTCCTTGAGCATGAACTTCTCACTGTGCCTTTCATGACTGGAGTCAATAATAATGAAGGT 1040
                                                                                                                                                                                                                                             GAGTTAAGGTATCCTTTAATCACCGATGGATATTTCCTCAAAAAATCAGCAGAGAAGTTG
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-----TTCCTGTCTGTGTTCTATCCT 1133

GACAAATATCTCCTCTTCACCCAGACCCCCCA 1646
TCACCCAGACCCCCCCA
ProArgValAspPheTrpThrSerThrIlePro
ACGGAGGAGTACCTGGGAATTGATGCAAAGGAGCAGAATGTTTATCAGGGTTTGAAAAAA
ThrGluGlnTyrLeuGlnLeuAspLeuAsnMetSerLeuGlyGlnArgLeuLysGlu
TTTGCTCGCACAGGGTCTCCTAATGGACAGGGTCTTGTCCACTGGCCAAAGTATGGAGAA 1553
PheAlaArgThrGlyAsnProAsnGlyAsnAspLeuSerLeuTrpProAlaTyrAsnLeu 520
AGTGCGTGCACTGAAGAAGAGGAGCAGTTGACCCAAATCATGATGAGCTACTGGGGCAAC 1493
GluGlyAlaThrGluGluLysLeuLeuSerArgLysMetMetLysTyrTrpAlaThr
GAGATGAAATATTTTTCGTATTTGGGCTTTGTTTCACAGTTTCTCACATCAATCTAAGC 1433
AlaAspGluValArgPheValPheGlyGlyAlaPheLeuLysGlyAspIleValMetPhe
TTGCAGCATTCCCCCAGTTTTCTAAAGGATAAAAGATCAAGCTTTGTTAGGAGTGACCAT
PheArgHiBArgProGlnCyBPheGluAspThrLysProAlaPheValLysAlaAspHis
CCTGCCATTAAGGCTGCTATTGCTCACAGAGATGCAGGTGCTCCTGTGTACCTGTATGAG
ProAlaLeuIleThrAlaArgTyrHisArgAspAlaGlyAlaProValTyrPheTyrGlu
GATCGTGTGAAAAACAGAGACGGGTACACTGAGGTGCTTGGAGACATGATATTTGTCATT
SerLeuThrGluIleArgAspSerLeuLeuAspLeuLeuGlyAspValPhePheValVal
GATCCCAAAGATGAGCAGCTTAGAAAACGGATTCTTAATGAATATACAGGAACTGGGGAG 1193
ProProGlnTyrLeuHisLeuValAlaAsnGluTyrPheHisAspLysHis 400

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Patent No. 6664091
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A. J.
APPLICANT: Silos-Santiago, Inmaculada
ITILE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
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ITILE OF INVENTION: 54011, A NOVEL HUMAN CARBOXYLESTERASE
ITILE OF INVENTION NUMBER: 08/10/023,515
CURRENT APPLICATION NUMBER: 2001-12-18
PRIOR APPLICATION NUMBER: 60/256,369
PRIOR APPLICATION NUMBER: 60/279,508
PRIOR APPLICATION NUMBER: 60/279,508
PRIOR FILING DATE: 2001-03-28
INMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
                                               ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (96).
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Alignment Scores
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REFERENCE: CLO01307 IT APPLICATION NUMBER: US/09/949,016 IT FILING DATE: 2000-04-14 APPLICATION NUMBER: 60/241,755 FILING DATE: 2000-10-20 APPLICATION NUMBER: 60/237,768 FILING DATE: 2000-10-03 APPLICATION NUMBER: 60/231,498 FILING DATE: 2000-09-08	281 AlaHisPheCysGlyAsnAsnAlaSerAspSerGluAlaLeuLeuArgCysLeuArgThr 30 281 AlaHisPheCysGlyAsnAsnAlaSerAspSerGluAlaLeuLeuArgCysLeuArgThr 30
Sequence 3799, Application US/09949016 ; Patent No. 6812339 ; GENERAL INFORMATION: ; APPLICANT: VENTER, J. Craig et al. ; TITLE OF INVENTION: FOLYMORPHISMS IN KNOWN GENES ASSOCIATED ; TITLE OF INVENTION: WITH HIMAN DISEASE METHODS OF DETECTION AND USES THEREOF	OY
b BSULT 3	221 GlyAspProSerSerValThrIlePheGlyGluSerAlaGlyAlaIleSerValSerSer 24
Oy 561 SerProLeuSerSerLeuTherPheLeuSerLeuLeuGlnProPhePhePhePhePhePhePhePhePhePhePhePhePheP	Qy 201 AlapheLysAspGlnValAlaAlaLeuSerTrpValGlnLysAsnIleGluPhePheGly 220
541 ArgValAspPhoTrpThrSerThrIleFroLeulleLeuSerAlaSerAspMetLeulls	Oy 181 TyrArgLeuGlyIlePheGlyPhePheThrThrTrpAspGlnHisAlaProGlyAsnTrp 200
1656 ACTGAGCAGTACCTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCG	OY 161 SerIlePheAspGlySerAlaLeuAlaAlaTyrGluAspValLeuValValValValGln 180
501 PheAlaArgThrGlyAsnProAsnGlyAsnAspLeuserLeutrpProAlaTyrasnLeu	OY 141 GlySerLysLeuProValLeuValTrpPheProGlyGlyAlaPheLysThrGlySerAla 160
481 GluGlyAlaThrGluGluGluFysLeuLeuSerArgLysMecMetLysTyrTrpAlaThr	Oy 121 PheGlyValSerGluAspCysLeuTyrLeuAsnIleTyrAlaProAlaHisAlaAspThr 140
AlaAspeinvalArgenevalrheeityeiyalarheibentyeetyheepileeringireceringiricggregorgccorcorgaagggggacartgtratgtrc	Qy 101 LeuGlnAsnSerGluTrpLeuLeuLeuAspGlnHisMetLeuLysValHisTyrProLys 120
41 PheArgH.BArgProGInCyBPheGluABpinELyBProAlaPheValLyBAlaAspH18	GY 81 ProGlnProAlaSerProTrpAspAsnLeuArgGluAlaThrSerTyrProAsnLeuCys 100
421 ProAlaLettifeliatatargiyen.Bargabaladyanlarrovaliyenelyedin	QY 61 AsnValPheLeuGlyValProPheAlaAlaProProLeuGlySerLeuArgPheThrAsn 80
401 Serieuiniginileargaspserieuleuspleeuleugyyspysalrneyneyslivat	Oy 41 ThrArgLeuGlyTrpIleGlnGlyLyBGlnValThrValLeuGlySerProValProVal 60
1236 CTGCACATCCCCCCCCAGTATTTGCACCCTTGTGGCTAATGAATACTTCCATGACAAGCAC	Oy 21 LeuLeuGlyH1sArgGlnTrpGlyLysThrGlyProSerAlaGluGlyProGlnArgAsn 40
361 AlaProGluIleLeuSerGlySerAsnLygSerLeuAlaLeuHisLeuHisLeuIleGlaAsnIle	Qy 1 MetProGlnGlyLeuThrSerSerAlaSerGlnTrpCyePhePheLeuIleLeuGlnPro 20
1016 GATGGTGCTTTCCTAATGAGCCTCTAGATCTATTGTCTCAGAAAGCATTTAAAGCA 341 IleProSerIleIleGlyValAsmAsmHisGluCysGlyPheLeuLeuProMetLysGlu	3-515-2 (1-581) x US-10-023-515-1 (1-2158)
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SOFTWARE: FastSEQ for Windows Version
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CysGlyAsnAsnAlaSerAspSerGluAlaLeuLeuArgCysLeuArgThrLysproSer
                                                                                                                                     LeuGluAlaHisAspTyrGluLysSerGluAspLeu-----GlnValValAlaHisPhe
                                                                                                                                                                                    ATATCCCAAGGACTCTTCCACGGAGCCATCATGGAGAGTGGCGTGGCCCTCCTGCCCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspCysLeuTyrLeuAsnIleTyrAlaProAlaHisAlaAspThrGlySerLysLeuPro 145
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                                    CACAGGCTCCAGTTCTGGAAGAAGGCGCTGCCC
                                                   ProArgValAspPheTrpThrSerThrIlePro
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                                                                                                         LeuThrGluGlnTyrLeuGlnLeuAspLeuAsnMetSerLeuGlyGlnArgLeuLysGlu 539
                                                                                       CAGGAGGAGCAATACCTGCAGCTGAACCTACAGCCTGCGGTGGGCCGGGCTCTGAAGGCC 1652
                                                                                                                                               AACTTTGCGAGAAATGGGAACCCCAATGGCGAGGGTCTGCCACACTGGCCGCTGTTCGAC
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GAGGAGATTCTTGCAATTAACAAGCCTTTCAAGATGATCCCCGGAGTGGTGGATGGGGTC 1007
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CTGCTGATGTTGCCTCCTACATTTGGTGACCTGCTGATGGGAGAGGAGAAT 1247
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US-09-949-016-555

Sequence 555, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: MUTH-HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-9-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

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; LENGTH: 2169
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-555
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                                                                                                                                         MetAlaLysGlyLeuPheHisLysAlaIleMetGluSerGlyValAlaIleIleProTyr
                                                                                                                                                                                                                                                                                                              SerAlaLeuAlaAlaTyrGluAspValLeuValValValValGlnTyrArgLeuGlyIle
    LysGluLeuLeuThrLeuSerGlnLysThrLysSerPheThrArgValValAspGlyAla 323
                                      ValThrIlePheGlyGluSerAlaGlyAlaIleSerValSerSerLeuIleLeuSerPro
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                                                     CysGlyAsnAsnAlaSerAspSerGluAlaLeuLeuArgCysLeuArgThrLysProSer
                                                                                                       LeuGluAlaHisAspTyrGluLysSerGluAspLeu-----GlnValValAlaHisPhe
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                                                                                  CTCATTGCC-----AGCTCAGCTGATGTCATCTCCACGGTGGTGGCCAACCTG
                                                                                                                                                                         GTCACCATTTTTGGCGAGTCTGCGGGTGGCACGAGTGTGTCTTCGCTTGTTGTGTCCCCC
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Mismatches:
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GENERAL INFORMATION:
APPLICANT: Danks, Mary K.
APPLICANT: Potter, Philip M.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Tumor Cells
FILE REFERENCE: SJ-0005
CURRENT APPLICATION NUMBER: US/09/595,682B
CURRENT APPLICATION NUMBER: 00/075,258
FRIOR APPLICATION NUMBER: 60/075,258
PRIOR FILING DATE: 1999-02-19
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR PILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 2191
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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                                          LysGluLeuLeuThrLeuSerGlnLysThrLysSerPheThrArgValValAspGlyAla 323
                                                                                     CysGlyAsnAsnAlaSerAspSerGluAlaLeuLeuArgCysLeuArgThrLysProSer 303
                                                                                                                                                                    ATATCCCAAGGACTCTTCCACGGAGCCATCATGGAGAGTGGCGTGGCCCTCCTGCCCGGC
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                     GAGGAGATTCTTGCAATTAACAAGCCTTTCAAGATGATCCCCGGAGTGGTGGATGGGGTC 1029
                                                                      LeuGluAlaHisAspTyrGluLysSerGluAspLeu-----GlnValValAlaHisPhe
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                                                                                                                                                                                                                                                                                                                                  TCCATGCTGGCTGGCTTGGAGAACGTGGTGGTGGTCATCATCCAGTACCGCCTGGGTGTC
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APPLICANT: Danks, Mary K.
APPLICANT: Potter, Philip M.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods :
TITLE OF INVENTION: Tumor Cells
FILE REFERENCE: SJ-0005
CURRENT APPLICATION NUMBER: US/09/595,682B
CURRENT FILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: 60/075,258
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
Alignment Scores:
                                        US-09-595-682B-20
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US-09-595-682B-20
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SEQ ID NO 20
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GENERAL INFORMATION:
                                                     LENGTH: 1717
TYPE: DNA
ORGANISM: Oryctolagus cuniculus
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DB:
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                                                 GAGAAAATTGCCATCGAAGCTGGGTGTAAAACCACCACCTCGGCTGTCATGGTTCACTGC
                                                                           GlnValValAlaHisPheCysGlyAsnAsnAlaSerAspSerGluAlaLeuLeuArgCys
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                                                                                                                            ValAlaIleIleProTyrLeuGluAlaHisAspTyrGluLysSerGluAsp-----Leu
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CTGCGCCAGAAGACAGAAGAACTCATGGAGGTGACATTGAAAATGAAATTTATGGCT
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                               APPLICANT: Feng, Paul C.C.

APPLICANT: Ruff, Thomas G.

TITLE OF INVENTION: Engineering Plant Resistance to Pyridines via TITLE OF INVENTION: Expression of Esterase Enzymes FILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance CURRENT APPLICATION NUMBER: US/09/264,737A CURRENT FILING DATE: 1999-03-09

EARLIER APPLICATION NUMBER: 60/077,377

EARLIER APPLICATION NUMBER: 60/077,377

EARLIER FILING DATE: 1998-03-10

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3
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; LENGTH: 1701 ; TYPE: DNA ; ORGANISM: Rabbit US-09-264-737-3

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                                             RESULT 7
US-09-264-737-3
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Sequence 3, Application US/09264737A Patent No. 6107549
GENERAL INFORMATION:
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                                                                                                                LeuAsnMetSerLeuGlyGlnArgLeuLysGluProArgValAspPheTrpThr 546
                                                                                                                                                                         GlyAsnAspLeuSerLeuTrpProAlaTyrAsnLeuThrGluGlnTyrLeuGlnLeuAsp
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      HisPheCysGlyAsnAsnAlaSerAspSerGluAlaLeuLeuArgCysLeuArgThrLys 301
                                                                                                                     ProTyrLeuGluAlaHisAspTyrGluLysSerGluAsp-----LeuGlnValValAla
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                                                                                              TCCAGTCTC-----TTCAGGÀAGAACACCAAGTCCTTGGCTGAGAAAATTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerGluAspCysLeuTyrLeuAsnIleTyrAlaProAlaHisAlaAspThrGlySerLys 143
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Patent No. 6783969
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
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                                                           Zhang, Jie
Xue, Aidong J.
Zhao, Qing A.
Wang, Jian-Rui
Chen,
Wang,
Wang,
                                                                                                                 Zhou, Ping
Goodrich, Ryle
Asundi, Vinod
Ren, Feiyan
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                                     Wang, Jian-Rui
Ma, Yunqing
Yamazaki, Victoria
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Zhiwei
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)..(925)
US-09-799-451-155
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APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Reena
APPLICANT: Ghosh, Reena
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6783969el Nucleic Ac:
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 155
LENGTH: 965
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                GluSerAlaGlyAlaIleSerValSerSerLeuIleLeuSerProMetAlaLysGlyLeu
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                                                                             TrpValGlnLysAsnIleGluPhePheGlyGlyAspProSerSerValThrIlePheGly
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SEQ ID NO 2515
LENGTH: 2802
TYPE: DNA
ORGANISM: Human
US-09-949-016-2515
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILLE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-01-03
PRIOR FILING DATE: 2000-01-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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                                 CCGATCGGCGAGAAACGTTTCCTGCCCCCTGAACCACCCCCATCCTGGTCGGGCATCCGG
                                                                                                                            ThrValLeuGlySerProValProValAsnValPheLeuGlyValProPheAlaAlaPro
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1015 ATCAAGTTCATGTATACAGACTGGGCAGACCGTGACACCCTGAGACCCGCGTAAA 1671 408 SerLeuLeuAspLeuLeuGlyAspValPhoPheValValProAlaLeuIleThrAlaArg 427 ::: ::: ::: :::	355 LEULGHPROMETLYSGINALAPROGINITELEUSEFGLYSERASHLYSSERLEUALALEU 374 ::: 1495 GTGGAAGGGGTGGTGGACCCTGAGGATGGTGTCTCTGGCACTGACTTTGACTATTCCGTC 1554 375HisteulleGlnAsnileLeuHisIleProPro	CARAGAGTGCCAAGGAGCTGGTAGAGCAGGACATCCAGGCCAGCGAGGCCACGTGGCC PheThrArgValValAspGlyAlaPhePheProAsnGluProLeuAspLeuLeuSerGln	240 SerLeuIleLeuSerProMetAlaLysGlyLeuPheHisLysAlaIleMetGluSerGly 259 1141 CTCCTCACGTTGTCACATCACTCAGAGGGGACTTTTCCAGAGAGCCATCATCCATAGTGGC 1200 260 ValAlaIleIleDroTyrLeuGluAlaHisAspTyrGluLysSerGluAspLeuGlnVal 279	200 TrpAlaPheLysAspGlnValAlaAlaLeuSerTrpValGlnLysAsnIleGluPhePhe 219 :::		142 Serlys	607 AACĠĊĠĊĠCACTTTĊĊĊCCAĠŢĠĠĊCCCĊĠĠĠĠĠCATCCACACAGGTGTGCCCGAAGTC 666 106TrpLeuLeuLeuAspGlnHisMetLeuLysValHisTyrProLysPhe 121 116	
US-10-023-515-2 (1-581) x US-09-949-016-1017 (1-4960) QY	Alignment Scores: Pred. No.: 5.99e-83 Length: 4960 Score: 789.50 Percent Similarity: 51.32% Conservative: Conservative: 107 Best Local Similarity: 33.72% Mismatches: Query Match: 4 Gaps: 22	PRIOR FILING DATE: 50/237,768 PRIOR FILING DATE: 2000-10-03 PRIOR APPLICATION NUMBER: 60/231,498 PRIOR TILING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 207012 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1017 LENGTH: 4960 TYPE: DNA ORGANISM: Human US-09-949-016-1017	9-016-1017 9-016-1017 NO. 6812339 L INFORMATION: CANT: VENTER, J. Cra OF INVENTION: POLYM OF INVENTION: WITH REFERENCE: CL001107 NT APPLICATION NUMBE: APPLICATION NUMBE: APPLICATION NUMBE: APPLICATION NUMBE: APPLICATION NUMBE: APPLICATION NUMBE: APPLICATION NUMBE: APPLICATION NUMBE:	531 MetSerLeuGlyGlnArgLeuLysGluProArgValAspPheTrpThrSerThrIlePro ::::::::::::::::::::::::::::::::::::	Qy 507 ProAsn	Qy 468 PheGlyGlyAlaPheLeuLy8GlyAspIleValMetPheGluGlyAlaThrGluGlu 486	Db 1672 ACACTGGTGGCACTCTTCACTGACCACCAGTGGTGGAGCCCTCAGTGGTGACAGCCGAT 1731 Qy 428 TyrHisArgAspAlaGlyAlaProValTyrPheTyrGlubheArgHisArgProGlnCys 447	1673 3030

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                                 GCTAGTGATTTTGACTTTGCTGTTTCAAATTTTGTTGATAATTTATATGGATATCCTGAA 1950
                                                         GlySerAsnLysSerLeuAlaLeu---HisLeuIleGlnAsnIleLeuHisIleProPro 385
                                                                                                                                                                                                  GluProLeuAspLeuLeuSerGlnLysAlaPheLysAlaIleProSerIleIleGlyVal 347
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                                                                                                   AACCAAGGGGAAGGGTTAAAATTTGTTGAAAATATAGTAGATAGCGATGATGGTATATCA
                                                                                                                                 AsnAsnHisGlu---CysGlyPheLeuLeuProMetLysGluAlaProGluIleLeuSer 366
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--GlnTyrLeuHisLeuValAlaAsnGluTyrPheHisAspLys 399
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Alignment Scores:
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Sequence 2516, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                            2599 GTACCTGTCACGTCAGCCTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2128 GCCTTTTACCAT-----CATTGCCAAACAGATCAGGTTCCAGCTTGGGCTGATGCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2008 CATAACCCTGAAACCAGAAGAAAAGACATTACTGGCTTTGTTTACGGACCATCAGTGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValProAlaLeuIleThrAlaArgTyrHisArgAspAlaGlyAlaProValTyrPheTyr 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTTATCTCCATATTGGATTAAAACCAAGAGTTAAAGAACATTACAGAGCCAATAAGGTG
                                                                                                                                                                                                                                                                            -----GlnProPhe 575
                                                                                                                                                                                                                                                                                                                                         TCTACAACAACTAAAGTGCCATCAACTGACATCACTTCAGACCTACGAGAAAAAATTCT 2598
                                                                                                                                                                                                                                                                                                                                                                                                          oLeuSer---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACCTCTGGTTGGAGTTGGTACCTCATCTGCATAATCTCAATGACATTTCTCAGTATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AspPheTrpThrSerThrIleProLeuIleLeuSerAlaSerAspMet-LeuHisSerPr 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---TyrLeuGlnLeuAspLeuAsnMetSerLeuGlyGlnArgLeuLysGluProArgVal 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAAATTTTGCTAAAACTGGTGACCCAAATCAACCAGTCCCTCAAGACACGAAATTCATT 2358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaThrPheAlaArgThrGlyAsnProAsn-----GlyAsnAspLeuSerLeu--- 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACGGAGACGAGGTTCCCTATGTACTGGGAATCCCCCATGATT---GGCCCTACAGAGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HisAlaAspGluValArgPheValPheGlyGlyAlaPheLeuLy8GlyAspIleValMet 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlupheArgHisArgProGlnCysPheGluAspThrLysProAlaPheValLysAlaAsp 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCACCAGCTGTAGCCACAGCGGATCTTCACTCAAACTTTGGTTCACCTACGTACTTCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HisSerLeuThrGluIleArgAspSerLeuLeuAspLeuLeuGlyAspValPhePheVal 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTCCTTGCAATTTCTCCAAAAATGATGTGATGCTGAGTGCAGTTGTAATGACATACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pheGlu---GlyAlaThrGluGluGluLysLeuLeuSerArgLysMetMetLysTyrTrp 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----TrpProAlaTyrAsnLeuThrGluGln 523
                                                                                                                                                                                                                                                                                                                                                                                                       ----SerLeuThrPheLeuSerLeuLeu------
                                                                                                                                                                                                               2620
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```

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2516
LENGTH: 2862
TYPE: DNA
ORGANISM: Human
US-09-949-016-2516

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음 중 문 ક 뭐 ફ 뭐 S g ঠ 밁 ঠ 밁 ঠ 밁 ঠ 밁 8 밁 ঠ 밁 र् В ঠ 밁 ð 밁 र् 밁 ð

Db 1138 TTCGGGGGAGACCCCCGCCGGATCACTGTCTTTGGCTCGGGCATTGGTGCATCCTGCGTC 1197	PheGlyGluSerAlaGlyAlaIleSerVal	QY 199 AsnTrpAlaPheLysAspGlnValAlaAlaLeuSerTrpValGlnLysAsnIleGluPhe 218	1018 CTCAACTATCGGGTTGGAGTGCTAGGTTTCCTGAGTACTGGAGATCAGGCTGCCAAGGGC 1		159 SerA	39 AspThrGlySerLysLeuProValLeuValTrpPheProGlyGlyAlaPheLysThrGly	ດ :	138 -	Db 781 ATTTCCAAGGAATGCCCCGAAAGCCCCAACAAGAAAATTTTCTTACCAAAGGAAAATTTTCTACCAAGGAAATGCCCCCAAAGGAAAAGCCCCAACAAGAAAATTTTTCTTACCAAAGGAAAATTTTTCTTACCAAAGGAAAATTTTTTTT	724CCCAACGAAGAC	122 GlyValSerGluAgoCvaLeuTvrTenAgnTleTvrAlabroalauta	daL	::: :ccagtgtgcccccagaacatccacacagctgtgcccgaagtc	euGlnAenSerGlu 10	Qy 72 ProLeuGlySerLeuArgPheThrAsnProGlnProAlaSerProTrpAspAsnLeuArg 91 :::	496 GAGATCCTGGG	GCCCAGT	36 GlyProGlnArgAs	Db 376 AGCCTGTGCCTCACCTGTGGTTCCTCAGTTTGGCGCTGAGGGCCAGTACCCAGGGCCCA 435	w	26	OY 12 TrpCy8PhePheLeuIleLeuGlnProLeuLeuGlyHi8Arg 25	-10-023-515-2 (1-	25.40% Indels: 4 Gaps:	Pred. No.: 1.78e-82 Length: Score: 782.00 Matches: Percent Similarity: 46.65% Conservative: Best Local Similarity: 29.66% Mismatches: 224
Db 2200 ČČĆCACCTATACAACCTGCATĠAČATGTTCĊAC 2232 RESULT 12	Qy 550 ProLeuIleLeuSerAlaSerAspMetLeuHis 560	Db 2140 AAACCAAGGGTCCGAGATCATTACCGGGCCACTAAGGTGGCCTTTTGGAAACATCTGGTG 2199	2080	Db 2020 GATCCCAACAAGCCGGTCCCCCAGGACACCAAGTTCACTCAC	506	Qy 486 GluGluLysLeuLeuSerArgLysMetMetLysTyrTrpAlaThrPheAlaArgThrGly 505	1903	Qy 467 ValPheGlyGlyAlaPheLeuLysGlyAspIleValMetPheGluGlyAlaThrGlu 485	Qy 447 CysPheGluAspThrlysProAlaPheValLysAlaAspHisAlaAspGluValArgPhe 466 Open	Db 1789 GATCTGCATGCCCGCTACGCCTACCTACCTTCTACGCCTTCTATCATCAC 1842		Qy 407 AspSerLeuLeuAspLeuLeuGlyAspValPhePheValValProAlaLeuIleThrAla 426 Db 1729 AAAACAGTGGGGGCACTGTACTGACTGCACTGCACTGACTG	_	Qy 387 TyrLeuHisLeuValAlaAsnGluTyrPheHisAspLysHisSerLeuThrGluIleArg 406	QY 374 LeuHisLeuIleGlnAsnIleLeuHisIleProPro	<u> </u>	ω t	Qy 335 GlnLy8AlaPheLy8AlaIleProSerIleIleGlyValA8nAsnHisGluCysGly 353	P	OV 315 SerpheThrarqValValAerGivalaebankspacaGCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCA		Db 1312 CTGCTGGCAGACAAAGTGGGCTGTAATGTGCTGGACACCGTGGATATGGTGGACTGTCTT 1371	. 12	Qy 259 GlyValAlaIleIleProTyrLeuGluAlaHisAspTyrGluLysSerGluAspLeuGln 278	Qy 239 SerSerLeuIleLeuSerProMetAlaLysGlyLeuPheHisLysAlaIleMetGluSer 258

115 LysValHisTyrProLysPheGlyValSerGluAspCysLeuTyrLeuAsnIleTyrAla	Qy 105 Glu	CCATCCTGGTCGGGCATCCGGAACGCCACACAC	Qy 85 SerProTrpAspAsnLeuArgGluAlaThrSerTyrProAsnLeuCysLeuGlnAsnSer 104 .::	Qy 65 GlyValProPheAlaAlaProProLeuGlySerLeuArgPheThrAsnProGlnProAla 84 :::	Qy 49 LysGlnValThrValLeuGlySerProValProValAsnValPheLeu 64	ysThrGlyProSerAlaGluGlyProGl :: GGGCCAGTACCCAGGCCCAGCACCCA	Match: Indels: Indels: Gaps: 4 Gaps:	Pred. No.: 2.47e-81 Length: Pred. No.: 775.00 Matchee: Score: Percent Similarity: 70.42* Conservative: Rest Local Similarity: Rest Local Simil	INFORMATION: -356C-5	I LOCATION: (4197). (4197) OTHER INFORMATION: n is not determined NAME/KEY: misc feature I COCATION: (4220)	not	OTHER INFORMATION: n is not determined; NAME/KEY: misc feature; LOCATION: (4179)(4179)(4179)	; IOCATION: (3)(3) ; IOCATION: (3)(3) ; OTHER INFORMATION: n is not determined ; NAME/KEY: misc_feature ; CCCTTON: (4).71	TYPE: DNA ORGANISM: Homo sapiens PEATURE:		; PRIOR APPLICATION NUMBER: PCT/US99/09365 ; PRIOR FILING DATE: 1999-04-29 ; PRIOR FILING DATE: 1998-04-29 ; PRIOR FILING DATE: 1998-04-29	; FILE REFERENCE: 9465.6USII ; CURRENT APPLICATION UNMBER: US/09/491,356C ; CURRENT FILING DATE: 2000-01-26	3	; GENERAL INFORMATION: ; APPLICANT: Philibert, Robert A. ; APPLICANT: Ginns, Edward I.	US-09-491-356C-5 ; Sequence 5, Application US/09491356C
&			B &	–	H		Ογ Db 1	Qy Db 1	Qy Db 1	B 87	Qγ Db 1	B &	Оу рь 1	D	Qy 1	B 8	Db	Q	g Q	שמ
441 PheArgHisArgProGlnCysPheGluAspThrLysProAlaPheValLysAlaAspHis 460	:::::::		401 SerfeuThrGlulleArgAspSerfeuLeuAspLeuLeuGlyAspValPhePheValVal	AAGGACACCCTGCGAGAGACCATCAAGTTCATGTATACAGACTGGGCAGACCGTGAC	368 SETABILYBSETLEUALALEUHIBLEULLEGITABILLEGEUNIBELLEGETOFT 303	AsnHisGluCysGlyPheLeuLeuProMetLysGluAlaProGluIleLeuSerGly	329 ProLeuABpLeuLeuSerGlnLysAlaPheLysAlaIleProSerIleIleGlyValAsn 348 :::	309 LeuSerGlnLysThrLysSerPheThrArgValValAspGlyAlaPhePheProAsnGlu 328	293 AlaLeuLeuArgCysLeuArgThrLysDroSerLysGluLeuLeuThr 308 ::::::	273 LysSerGluAspLeuGlnValValAlaHisPheCysGlyAsnAsnAlaSerAspSerGlu 292	253 LygAlaIleMetGluSerGlyValAlaIleIleProTyrLeuGluAlaHisAspTyrGlu 272 ::: ::::: 1271 AGAGCCATCATCCAAAGTGGCTCTGCTCTGTCCAGCTGGGCTGTGAACTACCAA 1324	233 AlaGlyAlaIleSerValSerSerLeuIleLeuSerProMetAlaLysGlyLeuPheHis 252	213 GlnLybAsnIleGluPhePheGlyGlyAspProSerSerValThrIlePheGlyGluSer 232 :::	193 AspGlnHisAlaProGlyAsnTrpAlaPheLysAspGlnValAlaAlaLeuSerTrpVal 212	173 ABDVALLEUVALVALVALVALGINTYFÄRGLEUGIYILEDHEGIYDHEPHETHFTHTTFD 192	153 GlyAlaPheLysThrGlyScrAlaSerIlePheAsgGlyScrAlaLeuAlaAlaTyrGlu 1/2 :::::: ::: ::: 971 GGCTCTTACATGGAAGGGACAGGCAACATGATTGATTGGCAGCATCTTCGCCAGTTATGGC 1030	GATGAAGATGAAGACATCCGGGACAGTGGTGTGTTAAACCCGTCATGGTCTACATCCACGGA		135 ProAlaHiBAlaAspThrGlySerLyB	

Alignment Scores: Pred. No.: 1.02e-80 Length: 1845	; NAME/KEY: CDS ; LOCATION: 11842 US-07-732-962A-1	9.0	; LENGTH: 1845 base pairs ; TYPE: NUCLEIC ACID ; STRANDEDNESS: single	; TELEPAX: (212) 664-0525 ; TELEX: 422523 COOP UI ; INFORMATION COR SEQ ID NO: 1: SECURENCE TURNS TOTALS	; REGISTRATION NUMBER: 28,678 ; REFERENCE/DOCKET NUMBER: 39304/JPW/LSW ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: (212) 977-9550	; FILING DATE: 19910722 ; CLASSIFICATION: 435 ; ATTORNEY/AGENT INFORMATION: ; NAME: White, John P.	; SOFTWARE: Patentin Release #1.0, Version #1.25 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/07/732,962A	COMPUTER: FLODDY disk COPERATING SYSTEM: PC-DOS/MS-DOS	ZIP: 10112 COMPUTER READABI	; CITY: New York ; STATE: New York ; COUNTRY: USA	VENTION: EQUENCES:	Meir	<u>0</u> ~ ω	N	544 PheTrpThrSerThrTleDroIeuTleIensGgTCCGAGATCATTACCGGGCCACTY		Db 2093 ACCAAGGCCAACCGCTTTGAGGAAGTGGCCTGGTCCAAATACAATCCCCGAGACCAGCTC 2152		N	TGCTCAGTGCTGTCG	481	Db 1916 GGGGATGAAGTACCCTATGTTTTTGGGGTTCCTATGGTAGGCCCCACTGACCTTTTC 1972	Qy 461 AlaAspGluValArqPheValPheGlvGlvAlaPheLenivsGlvAsnTleValWerThe 100	1000
Db 868 CCAGGCGCACTGGTGGGAATGACACAGAGCTGGTAGCCTGCCTTCGGACACGACCA 924 Qy 303 SerLysGluLeuLeuThrLeuSerGlnLysThrLys 314	Db 808 GTGGCATGGGAĠĀĠGCCCGTCGCAGGGCCACGCAGCTGGCCACCTTGTGGGCTĠTCCT 867 Qy 285GlyAsnAsnAlaSerAspSerGluAlaLeuLeuArgCysLeuArgThrLyspro 302	268 AlaHisAspTyrGluLysSerGluAspLeuGlnValValAlaHigPheCys	Qy 248 LysGlyLeuPheHisLysAlaIleMetGluSerGlyValAlaIleIleProTyrLeuGlu 267 ::: ::: ::::: Db 748 CGGGCCTGTTCCACAGGGCCGTGCTGCAGAGCCGTGCCCCAATGGACCCTTGCCCCACG 807	Qy 228 IlePheClyGluSerAlaGlyAlaIleSerValSerSerLeuIleLeuSerProMetAla 247 :::	່ ຄ ນ	ഗ ⊢	508 GTACAGGCCGAGGAGGACTGTGCTGGTGTCCATGAACTACCGGGTGGGAAGCTTTGGCTTC	ш.	Qy 151 ProGlyGlyAlaPheLysThrGlySerAlaSerllePheAspGlySerAlaLeu 168		Qy 111 GlnHisMetLeuLysValHisTyrProLysPheGlyValSerGluAspCysLeuTyrLeu 130	91 ArgGluAlaThrSerTyrProAsnLeuCysLeuGlnAsnSerGluTrpLeuLeuLeuAsp 110	211 CCACCCATGGGACCCCGTCGCTTTCTGCCACCGGAGCCCAAGCAGCCTTGGTCAGGGGTG	Db 151 ATTCGCCTGAAGACCCCCGGGGGCCCTGTCTCTGCTTTCCTGGGCATCCCTTTGCGGAG 210 QY 71 ProProLeuGlySerLeuArgPheThrAsnProGlnProAlaSerProTrpAspAsnLeu 90	Qy 59	Db 92 CTGAGGGCCGGGAGGATGCAGAGCTG-CTGGTGACGGTGCGTGGGGGCCCGGCTGCGGGGC 150	Qy 41 ThrargLeuGlyTrpIleGlnGlyLysGlnValThrValLeuGlySerProVal 58	ם	41 21	Qy 1 MetProGlnGlyLeuThrSerSerAlaSerGlnTrpCysPhePheLeuIleLeuGlnPro 20	7-732-962A-1 (1-1845)	Dest Local Similarity: 33.72% Mismatches: 221 Query Match: 24.83% Indels: 82 DB: Gans: 22	764.50 Matches: 49.83% Conservative:	

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PCT-US92-06106-1
Sequence 1, Application PC/TUS9206106
GENERAL INFORMATION:
APPLICANT: Pischer, Meir
TITLE OF INVENTION: ENZYMATICALLY ACTIVE RECOMBINANT HUMAN
TITLE OF INVENTION: ACETYLCHOLINESTERASE AND USES THEREOF
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: John P. White, Esq.
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1486 TAÇACGGCAGAGAAAATCTTCGCCCAGCGACTGATGCGATACTGGGCCAACTTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1159 CGGCCGAGTTCCTGGCCGGGGTGCGGGTCGGGGTTCCCCAGGTAAGTGACCTGGCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1045 GCGGGAGACTTCCACGGCCTGCAGGTGCTGGTGGTGGTGAAGGATGAGGGCTCGTAT 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           335 GlnLysAlaPheLysAlaIleProSerIleIleGlyValAsnAsnHisGluCysGlyPhe 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnCysPheGluAspThrLysProAlaPheValLysAlaAspHisAlaAspGluValArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ArgThrGlyAsnProAsn-------GlyAsnAspLeuSerLeuTrpProAlaTyrAsn 519
||||||||:::||||||
cgcaCAggggATCCCAATGAGCCCCGAGACCCCCAGAGGCCCCACAATGGCCCCCGTACACG 1605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---ThrGluGluGluLysLeuLeuSerArgLysMetMetLysTyrTrpAlaThrPheAla 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTCTG---GTTTACGGGGCCCCAGGC---TTCAGCAAAGACAACGAGTCTCTCATCAGC 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LysGluProArgValAspPheTrpThrSerThrIleProLeuIleLeuSerAlaSerAsp ::: ||||||||||||:::|||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCACGCTC----TCCTGGCCCCTGTGGATGGGGGTGCCCCACGGCTACGAGATCGAG 1449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerPheThrArgValValAspGlyAlaPhePheProAsnGluProLeuAspLeuLeuSer 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leu---ThrGluGlnTyrLeuGlnLeuAspLeuAsn---MetSerLeuGlyGlnArgLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCATCTTTGGG-------ATCCCCCTGGACCCTCTCGAAAC 1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PheValPheGlyGlyAlaPheLeuLysGlyAspIleValMetPheGluGlyAla-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGGAGGCCCTGAGCGATGTGGTGGGCGACCACAATGTCGTGTGCCCCGTGGCCCAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
SOPTWARE: PACENTIN Release #1.0, Ve
SOPTWARE: PACENTIN ROLESSE #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UNMBER: PCT/US92/06106
FILING DATE: 1920722
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
REGISTRATION UNMBER: 28,678
REFERENCE/DOCKET NUMBER: 39304-B-PC
REGISTRATION UNMBER: 39304-B-PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEFAX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION:
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       ProGlyGlyAlaPheLysThrGlySerAlaSer-----IlePheAspGlySerAlaLeu 168
                                                                                                                                                                                                                                              GTAGACGCTACAACCTTCCAGAGTGTCTGCTACCAATATGTGGACACCCTATACCCAGGT
                                                                                                AsnIleTyrAlaProAlaHisAlaAspThrGlySerLysLeuProValLeuValTrpPhe 150
                                                                                                                                                                                                                                                                            ArgGluAlaThrSerTyrProAsnLeuCysLeuGlnAsnSerGluTrpLeuLeuLeuAsp
                                                      AACGTGTGGACACCATACCCCCGGCCTACA---TCCCCCACCCCTGTCCTCGTCTGGATC
                                                                                                                                                  TTTGAGGGCACCGAGATGTGGAACCCCAACCGTGAGCTGÁGCGÁGGÁCTGCCTGTÁCCTC
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                                                                                                                                                          GlnCysPheGluAspThrLysProAlaPheValLysAlaAspHisAlaAspGluValArg 465
---ThrGluGluGluLysLeuLeuSerArgLysMetMetLysTyrTrpAlaThrPheAla 502
                                                 TTCATCTTTGGG-----------ATCCCCCTGGACCCCTCGAAAC 1485
                                                                                                                                                                                                                             AlaArgTyrHisArgAspAlaGlyAlaProValTyrPheTyrGluPheArgHisArgPro 445
                                                                                                                                                                                                                                                                    LeuLeuProMetLysGluAlaProGluIleLeuSerGlySerAsnLysSerLeu-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                AlaLeuHisLeuIleGlnAsnIleLeuHisIleProGlnTyrLeuHisLeuValAla
                                                                                      PheValPheGlyGlyAlaPheLeuLysGlyAspIleValMetPheGluGlyAla-----
                                                                                                                                                                                               GCTGGGCGACTGGCTGCCCAGGGTGCCCGGGTCTACGCCTACGTCTTTGAACACCGTGCT 1395
                                                                                                                                                                                                                                                                                                          ArgAspSerLeuLeuAspLeuLeuGlyAspValPhePheValValProAlaLeuIleThr 425
                                                                                                                                                                                                                                                                                                                                                                                                                     CGGGCCGAGTTCCTGGCCGGGTGCGGGTTCCCCCAGGTAAGTGACCTGGCAGCC
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CGGGGCCTGTTCCACAGGGCCGTGCTGCAGAGCGGTGCCCCAATGGACCCTGGGCCACG
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Best Local Similarity:
Query Match:
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US-09-949-016-1192
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US-09-949-016-1192
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LENGTH: 2158
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US-10-023-515-2 (1-581) x US-09-949-016-1192 (1-2158)
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PPLICATION NUMBER: 60/231,498
PRIOR PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASCSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1192, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                              135 CTTCCCCACTCCTTCTCCTCCTCTGGCTCCTGGGTG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetProGlnGlyLeuThrSerSerAlaSerGlnTrpCysPhePheLeuIleLeuGlnPro
CCACCCATGGACCCCGTCGCTTTCTGCCACCGGAGCCCAAGCAGCCTTGGTCAGGGGTG 364
                                                                                                    ATTCGCCTGAAGACCCCCGGGGGGGCCCTGTCTCTCTGCTTTCCTGGGCATCCCCTTTGCGGAG 304
                                                                                                                                                                                                                                                                                                                                                                       LeuLeuGlyHisArgGlnTrpGlyLysThrGlyProSerAlaGluGlyProGlnArgAsn
                                                  ProProLeuGlySerLeuArgPheThrAsnProGlnProAlaSerProTrpAspAsnLeu 90
                                                                                                                                                                                                                CTGAGGGCCGGGAGGATGCAGAGCTG-CTGGTGACGGTGCGTGGGGGCCGGCTGCGGGGC
                                                                                                                                                                                                                                                                ThrArqLeuGlyTrpIleGlnGlyLysGlnValThrValLeuGlySerProVal-----
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485 AACGTGTGGACACCATACCCCCGGCCTACA---TCCCCCACCCCTGTCCTCGTCTGGATC 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 ProGlyGlyAlaPheLysThrGlySerAlaSer-----IlePheAspGlySerAlaLeu 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlnLysAlaPheLysAlaIleProSerIleIleGlyValAsnAsnHisGluCysGlyPhe 354
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                                                                                                             GAGGCTGTGGTCCTGCATTACACAGACTGGCTGCATCCCGAGGACCCCG---GCACGCCTG 1369
                                                                                                                                                                                                                                                                                                                         TTTCTG---GTTTACGGGGCCCCAGGC---TTCAGCAAAGACAACGAGTCTCTCATCAGC 1252
                                                                                                                                                                                                                                                                                                                                                                                LeuLeuProMetLysGluAlaProGluIleLeuSerGlySerAsnLysSerLeu---- 372
                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGGGAGACTTCCACGGCCTGCAGGTGCTGGTGGTGGTGAAGGATGAGGCTCGTAT 1198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCGCAGGTCCTGGTGAACCACGAATGGCACGTGCTGCCTCAAGAAAGCGTCTTCCGGTTC 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerLysGluLeuLeu----- 314
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CGGGGCCTGTTCCACAGGGCCGTGCTGCAGAGCGGTGCCCCCAATGGACCCTGGGCCACG 901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaLeuSerTrpValGlnLysAsnIleGluPhePheGlyGlyAspProSerSerValThr 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PheThr---ThrTrpAspGlnHisAlaProGlyAsnTrpAlaPheLysAspGlnValAla 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaAlaTyrGluAspValLeuValValValValGlnTyrArgLeuGlyIlePheGlyPhe 188
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                                                ArgAspSerLeuLeuAspLeuLeuGlyAspValPhePheValValProAlaLeuIleThr 425
                                                                                                                                                                                                                    CGGGCCGAGTTCCTGGCCGGGGTGCGGGTCGGGGTTCCCCCAGGTAAGTGACCTGGCAGCC 1312
                                                                                                                                                                                                                                                                     AlaLeuHisLeuIleGlnAsnIleLeuHisIleProProGlnTyrLeuHisLeuValAla 392
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AGGGAGGCCCTGAGCGATGTGGGGCGACCACAATGTCGTGTGCCCCGTGGCCCAGCTG 1429
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1820 ACCCTC 1825
                                     558 MetLeu 559
                                                                        CGCGCCCAGGCCTGCGCCTTCTGGAACCGCTTCCTCCCCAAATTGCTCAGCGCCACCGAC 1819
                                                                                                                                                                                                                                                                                                                        ---ThrGluGluLysLeuLeuSerArgLysMetMetLysTyrTrpAlaThrPheAla 502
                                                                                                                                                 GCGGGGGCTCAGCAGTACGTTAGTCTGGACCTGCGGCCGCTGGAAGGTGCGGCGGGGGCTG 1759
                                                                                                                                                                                Leu---ThrGluGlnTyrLeuGlnLeuAspLeuAsn---MetSerLeuGlyGlnArgLeu 537
                                                                                                                                                                                                                                                                                                      TACACGGCAGAGGAGAAAATCTTCGCCCAGCGACTGATGCGATACTGGGCCAACTTTGCC 1639
                                                                                                                                                                                                                                                                                                                                                                                                                    PheValPheGlyGlyAlaPheLeuLysGlyAspIleValMetPheGluGlyAla----- 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCACGCTC----TCCTGGCCCCTGTGGATGGGGGTGCCCCACGGCTACGAGATCGAG 1543
                                                                                                           LysGluProArgValAspPheTrpThrSerThrIleProLeuIleLeuSerAlaSerAsp 557
                                                                                                                                                                                                                                                             ArgThrGlyAsnProAsn------GlyAsnAspLeuSerLeuTrpProAlaTyrAsn 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlnCysPheGluAspThrLysProAlaPheValLysAlaAspHisAlaAspGluValArg 465
                                                                                                                                                                                                                             CGCACAGGGGATCCCAATGAGCCCCGAGACCCCAAGGCCCCACAATGGCCCCCGTACACG 1699
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Search completed: June 15, 2005, 13:34:22 Job time: 331 secs

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Post-processing: Minimum Match 0%
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1 /cgn2 6/ptcdata/1/pubpna/USO7_PUBCOMB.seq:*

2 /cgn2-6/ptcdata/1/pubpna/PCT_NEW_PUB.seq:*

3 /cgn2-6/ptcdata/1/pubpna/USO6_NEW_PUB.seq:*

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Sequence 45, Appl
Sequence 23, Appl
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ALIGNMENTS

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APPLICANT: CUTTIE, ROTY A. J.

APPLICANT: Silos-Santiago, Inmaculada

ITITLE OF INVENTION: 53010, A MOVEL HUMAN CARBOXYLESTERASE

ITITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF

FILE REFERENCE: 10448-122001

CURRENT APPLICATION NUMBER: US/10/023,515

CURRENT FILING DATE: 2001-12-18

PRIOR APPLICATION NUMBER: 60/256,369

PRIOR APPLICATION NUMBER: 60/256,369

PRIOR APPLICATION NUMBER: 60/279,508

PRIOR APPLICATION NUMBER: 60/279,508

PRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NOS: 1
                                                                                                        ; LENGTH: 2158
; TYPE: DNA
; ORGANISM: Homo mapiens
; PEATURE:
; NAME/KEY: CDS
; LOCATION: (96)...(1838)
US-10-023-515-1
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US-10-023-515-1
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Publication No. US20020182636A1
GENERAL INFORMATION:
Query Match 100.0%; Score 2158; Best Local Similarity 100.0%; Pred. No. 0; Matches 2158; Conservative 0; Mismatches
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Sequence 1, Application US/10674636

Publication No. US20040086922A1

GENERAL INFORMATION:

APPLICANT: Curtis, Rory A. J.

APPLICANT: Silos-Santiago, Inmaculada

ITILE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE

ITILE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE

ITILE OF INVENTION: FAMILY MEMBER AND USES THEREOF

FILE REFERENCE: 10448-122001

CURRENT APPLICATION NUMBER: US/10/674,636

CURRENT FILING DATE: 2003-19-19

PRIOR APPLICATION NUMBER: US/10/023,515

PRIOR APPLICATION NUMBER: 06/256,369

PRIOR APPLICATION NUMBER: 60/256,369

PRIOR APPLICATION NUMBER: 60/279,508

PRIOR APPLICATION NUMBER: 60/279,508

PRIOR PILING DATE: 2000-13-28

NUMBER OF SEQ ID NOS: 6

SOPTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 2158

TYPE: DNA

ORGANISM: Homo sapiens

PEATURE:

NAME/KEY: CDS

LOCATION: (1838)
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APPLICANT: KAICHEL, Venkateswarlu
APPLICANT: KICHEL, Venkateswarlu
APPLICANT: KILOS-Santiago, Inmaculada
APPLICANT: KILOS-Santiago, Inmaculada
APPLICANT: KILOS-Santiago, Inmaculada
APPLICANT: KILOS-Santiago, Inmaculada
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: MOLOCICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
TITLE OF INVENTION: 1045, 636, 4421, 5410, 30905, 2045, 14405, 1850, 2047,
TITLE OF INVENTION: 33751, 52872, 14063, 2077, 22245, 2287, 52908, 69112, 14930,
TITLE OF INVENTION: 33751, 52872, 14063, 2077, 22245, 2287, 52504, 6875,
TITLE OF INVENTION: 18547, 115, 579, 1598, 15622, 760, 18601, 2395, 2554, 6875,
TITLE OF INVENTION: 2548, 8263, 15402, 15827, 32620, 577, 619, 1423,
TITLE OF INVENTION: 2543, 9626, 13231, 32678, 21165, 30911, 41897, 1433,
TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
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APPLICANT: SANJANWALA, Madhusudan M.; YAO, Monique G.
APPLICANT: AU-YOUNG, Janice K.; BAUGHN, Mariah R.
APPLICANT: LEE, Ernestine A.; DING, Li
APPLICANT: LEE, Ernestine A.; DING, Li
APPLICANT: HAFALIA, April J.A.; TANG, Y. Tom
APPLICANT: LU, Dyung Aina M.; LAL, Preeti G.
APPLICANT: LU, Dyung Aina M.; LAL, Preeti G.
APPLICANT: WARREN, Bridget A.; YANG, Jumming
APPLICANT: GANDHI, Ameena R.; LU, Yan
APPLICANT: ISON, Craig H.
TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
FILE REFERENCE: FI-0313 USN
CURRENT APPLICATION NUMBER: US/10/433,256
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: PCTUSO1/47429
PRIOR APPLICATION NUMBER: US 60/254,308
PRIOR APPLICATION NUMBER: US 60/254,308
PRIOR APPLICATION NUMBER: US 60/257,713
PRIOR APPLICATION NUMBER: US 60/257,713
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PRIOR APPLICATION NUMBER: US 60/257,713
PRIOR APPLICATION NUMBER: US 60/262,706
PRIOR APPLICATION NUMBER: US 60/267,706
PRIOR APPLICATION NUMBER: US 60/267,706
PRIOR PILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/266,020
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PERL Program
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                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 23
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 6538080CB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23, Application US/10433256 Publication No. US20040081980A1 GENERAL INFORMATION:
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Best Local Similarity 99.5%;
Matches 1959; Conservative
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Sequence 249, Application US/10104047

Publication No. US20030236392A1

GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
ITILE OF INVENTION: No. US20030236392A1e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2002-03-25

PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 249
LENGTH: 2092
TYPE: DNA
ORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/10/023,515 ; CURRENT FILING DATE: 2001-12-18 ; PRIOR APPLICATION NUMBER: 60/256,369 ; PRIOR FILING DATE: 2000-12-18	; TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOATIESTERASE ; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF ; FILE REFERENCE: 10448-122001	GENERAL INFORMATION: APPLICANT: Curtis, Rory A. J. APPLICANT: Silos-Santiago, Inmaculada TETEL CE INFORMATION:	RESULT 6 US-10-023-515-3 ; Sequence 3, Application US/10023515 · bublication No US2002018263681	Cy 2096 GGITTTGTAACTCATATGAAATAAAATCAGAATGT 2130 Db 2056 GGTTTTGTAACTCATATGAAATAAAATCAGAATGT 2092	1998 GCCAACAAGATTTCCTCAATAATTTGGAAGAGGGCTGGCCTATTAGTTGTCATAATTAAT	1938	1916 GCTCAGCTICCTITCTATGGGGATCCTTGCAAAACAAGCTGCTTTTCGCTGATATTTTATGG	1030 GIGAIII IGGIIICCCIICCIANAII CICCCGCAATCAICAICAGCIICIIICIGA [1/96 ITTCCTCTCCTCCAGCCTTTCTTTTTTTTTTTTGTGCTCCTTGAGAAGTTATCTTTCTT	1736 CACCATCCCCTGATCCTGTCTGTCTGCCTCGACATGCTCCACAGTCCTCTTTCTT	1676 GGACTTGAACATGAGCCTCGGACGAGAGCTCAAAGAAACCGCGGGTGGATTTTTGGACCAG	TAATGGAACGACTGTCTCTGGCCACTTATAATCTGACTGA	1556 GAAGTTACTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACCGGGAATCC	Db 1458 GTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGA 1517	1436 CTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGT 1398 CTTTGAAGACACGACGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGT 1398 CTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGT	13/6 ATATICACASAGATGCTGGTGCACCCTGTCTACTACTACTACTACTGCACCCCCCACTGCTGTGTGCACCTGCTCTATGAGTTTTCGGCACCGGCCTCAGTG	1278 CAGTCTTCTGGACTTGCTTGGAGATGTTGTTGTTGTGGTCCCTGCACTGATCACAGCTCG	Db 1218 TTTGCACCTTGTGGCTAATGAATACTTCCATGACAAGCACTCCCTGACTGA

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# PRIOR APPLICATION NUMBER: 60/279,508
# PRIOR FILING DATE: 2001-03-28
# NUMBER OF SEQ ID NOS: 6
# SOFTWARE: FASTSEQ for Windows Version 4.
# SEQ ID NO 3
# LENGTH: 1746
# TYPE: DNA
# ORGANISM: Homo sapiens
US-10-023-515-3
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Sequence 3, Application US/10674636
Publication No. US20040086922A1
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A. J.
APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-122001
CURRENT APPLICATION NUMBER: US/10/674,636
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CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: US/10/023,515
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/256,369
PRIOR APPLICATION NUMBER: 60/279,508
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
INTMBER: OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1746
TYPE: DNA
ORGANISM: Homo sapiens
US-10-674-636-3
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RESULT 8
US-10-451-168-40
; Sequence 40, Application US/10451168
; Publication No. US20040091969A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
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APPLICANT: SMITHKLINE BEECHAM p.1.c.
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50039

CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-17
PRIOR FILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR APPLICATION NUMBER: 60/266,997
PRIOR APPLICATION NUMBER: 60/266,997
PRIOR PRILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/266,997
PRIOR PILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/289,622
PRIOR TILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/289,622
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FRESSEQ for Windows Version 4.0
LENGTH: 1728
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-451-168-40
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Best Local Similarity 99.9%;
Matches 1654; Conservative (
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APPLICANT: OTSUKA, KAORU
APPLICANT: NACAI, KEIICHI
APPLICANT: TRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHIKO
APPLICANT: SEKI, NAOHIKO
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILL REFERENCË; 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT APPLICATION NUMBER: 06/350,435
PRIOR APPLICATION NUMBER: 06/350,435
PRIOR PILING DATE: 2002-01-24
PRIOR FILING DATE: 2002-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LENGTH: 1962
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-094-749-736
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APPLICANT: SUGIYAMA,
APPLICANT: SUGIYAMA,
APPLICANT: OTSUKI, T
APPLICANT: MAKAMATS;
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APPLICANT: SATO, HIR
APPLICANT: ISHII, SH
APPLICANT: YAMAMOTO,
APPLICANT: YAMAMOTO,
APPLICANT: OTSUKA, K
APPLICANT: IRIE, RYC
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OTSUKI, TETSUJI
WAKAMATSU, AI
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ISONO, YUUKO
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APPLICANT: Rothenberg, Mark E.
ITILE OF INVENTION: NO. US20040030110A1el Proteins and Nucleic Acids Encoding Same
CURRENT APPLICATION NUMBER: US/10/114,270
CURRENT APPLICATION NUMBER: 60/281,086
PRIOR APPLICATION NUMBER: 60/281,086
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR APPLICATION NUMBER: 60/281,863
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Publication No. US20040030110A1
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APPLICANT Gerlach, Valerie
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Shimkets, Richard A.
Gangolli, Esha A.
Taupier Jr., Raymond J.
Casman, Stacie J.
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Shenoy, Suresh G.
Pena, Carol E.A.
Smithson, Glennda
Burgess, Catherine E.
Gerlach, Valerie
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PRIOR APPLICATION NUMBER: 60/281,906

PRIOR APPLICATION NUMBER: 60/282,020

PRIOR FILING DATE: 2001-04-05

PRIOR FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: 60/282,930

PRIOR FILING DATE: 2001-04-10

PRIOR PRIOR FILING DATE: 2001-04-10

PRIOR PRIOR FILING DATE: 2001-04-12

PRIOR APPLICATION NUMBER: 60/283,512

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PRIOR FILING DATE: 2001-04-12

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; APPLICANT: SMITHKLINE BEECHAM p.l.c.
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PRIOR FILING DATE: 2001-03-19
PRIOR PELICATION NUMBER: 60/281,535
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/289,622
PRIOR FILING DATE: 2002-06-28
PRIOR FILING DATE: 2002-06-28
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US-10-451-168-41
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TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50039
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/US01/49232
PRIOR FILLING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR FILING DATE: 2000-12-20
PRIOR PILING DATE: 2000-12-20
PRIOR PILING DATE: 2001-01-02
PRIOR PILING DATE: 2001-01-09
PRIOR PILING DATE: 2001-01-09
PRIOR PILING DATE: 2001-01-09
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PRIOR PILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR APPLICATION NUMBER: 60/264,922
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                                                           ACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCC
                                                                                                                                                              TATGAGGACGTGCTGGTTGTGGTCGTCCAGTACCGGCTAGGAATATTTTGGTTTTCTTCACC
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1146 GAGTGTGGCTTCCTGCTGCTATGAAGGAGGCTCCTGAGATCCTCAGTGGCTCCAACAAG
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APPLICANT: LEE, Ernestine A.; LU, Preeti G.;
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APPLICANT: CHAMIA, Narinder K.; WALSH, Roderick T.;
APPLICANT: WARREN, Eridget; XU, Yuning
APPLICANT: WARREN, Eridget; XU, Yuning
APPLICANT: VANG, Junming; YAO, Monique; YUE, Henry
FILE REFERENCE: PI-023 USN
CURRENT APPLICATION NUMBER: US/10/381,898
CURRENT APPLICATION NUMBER: US/10/381,898
CURRENT APPLICATION NUMBER: US/0/236,947
PRIOR APPLICATION NUMBER: US 60/236,947
PRIOR APPLICATION NUMBER: US 60/236,947
PRIOR APPLICATION NUMBER: US 60/238,864
PRIOR APPLICATION NUMBER: US 60/247,581
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PRIOR PILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-11-30
NUMBER: US 60/247,581
PRIOR FILING DATE: 2000-11-30
NUMBER: US 60/247,581
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NUMBER: US 60/249,519
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NUMBER: US 60/249,519
PRIOR FILING DATE: 2000-11-30
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Best Local Similarity 94.7%;
Matches 1473; Conservative C
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Pred. No. 0;
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APPLICANT: Yamashita, Tetsuro
APPLICANT: Miyazaki, Masao
TITLE OF INVENTION: CAT KIDNEY DISEASE MARKER
FILE REFERENCE: SHIG FP02USO06
CURRENT APPLICATION NUMBER: US/10/233,933A
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: JP2002-057908
PRIOR APPLICATION NUMBER: JP2002-057908
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 4
SECTIMARE: Patentin Ver. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/10233933A Publication No. US20040214171A1 GENERAL INFORMATION:
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Best Local Similarity 78.2%;
Matches 1466; Conservative
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TYPE: DNA
ORGANISM: Felis catus
FEATURE:
NAME/KEY: CDS
LOCATION: (175)..(1803)
FEATURE:
NAME/KEY: misc feature
LOCATION: (1804)..(2145)
OTHER INFORMATION: n is a,
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Sequence 1, Application US/10233933A

Publication No. US20040214171A1

GENERAL INFORMATION:

APPLICANT: Yamashita, Tetsuro

APPLICANT: Miyazaki, Masao

ITILE OF INVENTION: CAT KIDMEY DISEASE MARKER

FILE REFERENCE: SHIG PPO2US006

CURRENT APPLICATION NUMBER: US/10/233,933A

CURRENT FILING DATE: 2002-09-03

PRIOR APPLICATION NUMBER: UF2002-057908

PRIOR FILING DATE: 2002-04-03

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin Ver. 2.0

LENGTH: 1629
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; ORGANISM: Felis
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AACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTC
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                                                                                                                    GACACGAGGCAGCTTTCGTGAAAGCCGATCACTCTGATGAAATCCGCTTCGTCTTTGGA 1380
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CTGAGCAGGAAGATGATGAGGTACTGGGCCAACTTTGCTCGGACCGGGGACCCTAACGG
                 CTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACCGGGAATCCTAATGGG
                                                                              GGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGAGGAGAAGTTA 1562
                                                                                                                                                 GACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTTTCGGT 1502
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TITLE OF INVENTION: NUMBER: US/10/451,168
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/US01/49232
PRIOR APPLICATION NUMBER: PCT/US01/49232
PRIOR FILING DATE: 2000-12-17
PRIOR PILING DATE: 2000-12-19
PRIOR PILING DATE: 2000-12-19
PRIOR PILING DATE: 2000-12-09
PRIOR PILING DATE: 2000-12-09
PRIOR PILING DATE: 2001-01-09
PRIOR PILING DATE: 2001-01-09
PRIOR PILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-03-19
PRIOR PILING DATE: 2001-03-19
PRIOR PILING DATE: 2001-04-04
PRIOR PILING DATE: 2001-04-04
PRIOR PILING DATE: 2001-04-04
PRIOR PILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 110
PRIOR PILING DATE: 2002-06-28
NUMBER: PSETER FOR THE MADER: 60/289,622
PRIOR PILING DATE: 2002-06-28
NUMBER: PSETER FOR THE MADER: 60/289,622
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; SEQ ID NO 42
; LENGTH: 1071
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-451-168-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 47.3%;
Best Local Similarity 99.9%;
Matches 1022; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SMITHKLINE BEECHAM CORPORATION APPLICANT: SMITHKLINE BEECHAM p.l.c. APPLICANT: GLAXO GROUP LIMITED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1623 AACGACCTGTCTCTGTGGCCAGCTTATAATCTGACTGAGCAGTACCTCCAGCTGGACTTG
  1059 GGTGCTTTCTTTCCTAATGAGCCTCTAGATCTATTGTCTCAGAAAGCATTTAAAAGCAATT 1118
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                                                                                     CCCTCCAAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACTCGAGTGGTTGAT 1058
                                                                                                                                                                             CATTTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAA
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                                                                                                                                                                                                                                                                                     ATCATCCCTTACCTGGAGGCCCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCA
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Search completed: June 15, 2005, 08:31:05 Job time : 1399.55 secs

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AB186392 Canis fam
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18.5	18.5	18.5	18.5	18.5	18.5	18.5	18.5	18.6	18.6		18.8	18.8	18.8		18.8	18.8	18.8		18.9	19.2	24.1	24.4	24.6	24.6	24.6
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ALIGNMENTS

8				.: Q	8	Ş	В	Ą	Query Match Best Local Sig Matches 2158;	ORIGIN	FEATURES	JOURNAL	TITLE	AUTHORS		ORGANISM	SOURCE	VERSION	ACCESSION	DEFINITION	AR438764	
241 AGCAAGTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCCTTTG 300		181 AAACTGGGCCTTCTGCTGAAGGGCCACAGAGGAACACCAGGCTGGGATGGAT	121 CTTCACAATGGTGCTTTTTCCTGATTCTCCAGCCCCTGTTGGGACACAGACAG	121 CTTCACAATGGTGCTTTTTCCTGATTCTCCAGCCCCTGTTGGGACACAGACAG	61 TTTAAAAATTATTCTTAATAAAAGTACGAATGCCACAGGGGACTTACTT	61 TTTAAAAATTATTCTTAATAAAAGTACGAATCCCAATGCCACAGGGACTTACTT	1 CCACGCGTCCGAAAAACAGGCCTGGAGAGCAATGTGGAGTAAGCAATGTAATAAAAACGA 60	1 CCACGCGTCCGAAAAAACAGGCCTGGAGAGCAATGTGGAGTAAGCAATGTAATAAAAACGA 60	/ Match 100.0%; Score 2158; DB 6; Length 2158; Local Similarity 100.0%; Pred. No. 0; nes 2158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/mol_type="genomic DNA"	Location/Qualitiers	: US 6664091-A 1 16-DEC-2003;	53010, a human carboxylesterase family member and uses thereof	Curtis, R.A.J. and Silos-Santiago, I.	• Ĕ		Unknown.	AR438764.1 GI:42663739	AR438764	AR438764 2158 bp DNA linear PAT 20-FEB-2004		

1081 CTCTAGATCTATTGTCTCAGAAAGCATTTAAAGCAATTCCTTCC	161 ACTTGCGAAAGACAAGGCCACATCAGTTCTAAGTTCTAAGATCCGAAATCCGAAGTCCTAGAGCCCCAAGGCCCCAAGACCCCTTCT 420 121 TAGATCAACACTGCTCAAGGTGCATTACCCGAAATTCGGAGTGCAGAAGACTGCTGCTCT 480 121 TAGATCAACACTGTATGCGCCTGCCCAAGACCAAGACTCCAAGAGCTCCAAGAGCTCCAAGAGCTCCCAAGACTGCCTCT 480 121 TAGATCAACACTGTATGCGCCTGCCCAAGACCAAGACTCCAAGAGTCCAAGAGCTCCAAGACTCCCTCT 480 121 TAGATCCAACACTGTATGCGCCTGCCCAAGACCAAGACCACCAAGACTCCAAGCTTCCAAGACTCCCCCTTCT 480 121 TAGATCCAACACTTTATGCGCCTGCCCAAGCCCGAAAACAAGCCTCCAAGCTTCCAAGACTTCCCCCGTCTTGGTGT 540 1481 ACCTGAACATCTTATGCGCCTCCAAGACCAGCCCCAAACAACAACTGCCCCAAGCTTCAAGACTTCCCCAAGCTTCAAGACTTCCCCCGTCTTGGTTGT 540 1481 ACCTGAACAATCTTATGCGCCTCAAGACTACACCTCCAACCTTTTGATGGGTCCCCCCCTTCGTGTTTGTT	241 AGCAAGTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCTTTG 300 301 CTGCTCCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATA 360
RESULT 2 AX600124 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE	Db 1441 Qy 1501 Qy 1561 Qy 1561 Qy 1621 Db 1621 Db 1681 Db 1681 Db 1681 Db 1741 Qy 1861 Db 1861 Qy 1921 Db 1921 Qy 1981 Qy 2041 Db 2041 Db 2101	
AX600124 AX600124 AX600124 AX600124.1 GI:28400190 . Homo sapiens (human) Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Curtis, R.A. and Silos-Santiago, I. 53010, a novel human carboxylesterase family member and uses thereof Patent: WO 0250256-A 1 27-JUN-2002; Millennium Pharmaceuticals, Inc. (US) Location/Qualifiers 12158	H-H 0-0 0-0 0-0 H-H 1 1 1	1381 ACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTGCTTTG 1440

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SIFDGSALAAYEDVLVVVQYRLGIFGFFTWDQHAPGWMAFKUQVAALSWVQKNIEF
FGGDPSSVTIFGESAGAISVSSLILSPWAKGLFHKAIMESGVAIIPYLEAHDYEKSED
LQVVAHFCGNNASDSBALLRCLATKESKELLTLSQKTKSFTRVVDAFFPNEPLDLLS
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NEYFHDKHSLTEIRDSLLDLLGDVFFVVPALITARYHRDAGAPVFFYEFAHTQNPN
REYFHDKHSLTEIRDSLLDLLGDVFFTVVPALITARYHRDAGAPVFFYEFAHTQNPN
GNDLSLWPAYNLTEQYLQDDLNNSLGQRLKEPRVDFWTSTIPLILSASDMLHSPLSSL
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416 GCTCTTAGATCAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTG 475	356 GGATAACTTGCGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCT 415 	296 CTTTGCTGCTCCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTG 355	236 GGCAAGCAAGTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCC 295 	176 GGGAAAAACTGGGCCTTCTGCTGAAGGGCCACAGAGGAACACCCAGGCTGGGATGGAT	Match 90.5%; Score 1953; DB 6; Length 2232; OCAL Similarity 99.5%; Pred. No. 0; 1959; Conservative 0; Mismatches 10; Indels 0; Gaps 0;	/mot_type="unabatgned numm" /db xref="taxon:9666" /note="Incyte ID No: 6538080CB1"		Walla,N.K., Nguyen,D.B., Gandhi,A.R. a Drug metabolizing enzymes Patent: WO 0246456-A 23 13-JUN-2002; Incyte Genomics Inc. (100)	1 Sanjanwala,M.M., Yao,M.G., Au-Young,J., Baughn,M.R., Ring,H.Z., Lee,E.A., Ding,L., Hafalia,A.J., Tang,Y.T. Triboulev.C.M. In D. T. Tang, T. T. T. T. T. T. T. T. T. T. T. T. T.	Homo sapiens (human) M Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini. Hominidae. Homo	N Sequence 23 from Patent W00246426. AX477711 AX477711.1 GI:22216866	3333	2101 TGTAACTCATATGAAATAAAATCAGAATGTAAAATAAGGAAAAAAAA	2041 CAAGATTTCTTCAATAAATTTGGAAGAGGGCTGGCCTATTAGTTGTCATAATAATGGTTT 2100	1981 GGAATGATCCTTACAGAATTCTTTTCAACATCAAAAAGTGCAATTTGTCTTGGAAGGCAA 2040 	1921 GCTGCTTTCTATGGGATCCTTGCAAAACAAGCTGCTTTCGCTGATATTTTATGGACTTA 1980 	1861 TTTGGTTTCCCTTCTCCCCATAATTTCTCCCGCAATCATTAGCTTCTTTCT	10
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1496 GTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGAGGA	1436 CTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGT	1376 ATATCACAGAGATGCTGGTGCACCTGTCTACTATGAGTTTTCGGCACCGGCCTCAGTG	0 4	1256 TTTGCACCTTGTGGCTAATGAATACTTCCATGACAAGCACTCCCTGACTGA	1196 CTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAACATCCTGCACATCCCGGCCTCAGTA	1136 CAATAACCACGAGTGTGGCTTCCTGCTGCCTATGAAGGAGGCTCCTGAGATCCTCAGTGG 	1076 TGAGCCTCTAGATCTATTGTCTCAGAAAGCATTTAAAGCAATTCCTTCC	1016 GACCCTCAGCCAGAAAACAAAGTCTTTCACTCGAGTGGTTGATGGTGCTTTCTTT	956 : IGGICAGACTCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAACCCTCCAAGGAGCTGCT 	96	836 CAAAGGCTTATTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGA 	776 CATCTTTGGCGAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGC		656 TTTCTTCACCACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGC		536 GGTGTGGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGAGLTCTTTGATGGGTCCGAGLTCTTTGATGGGTCCGAGCTCAGCCTCCATCTTTGATGGGTCCGAGCTCAGCCTCCATCTTTGATGGGTCCGAGCTCAGCCTCCATCTTTGATGGGTCCGAGCTCAGCTCAGCCTCCATCTTTGATGGGTCCGAGCTCAGCCTCCATCTTTGATGGGTCCGAGCTCAGCCTCCATCTTTGATGGGTCCGAGCTCAGCCTCCATCTTTGATGGGTCCGAGCTCAGCCTCCATCTTTGATGGGTCCGAGCTCAGAGAGTGCCGAGCTCAGCTTCAAGCTTCAGCTTCAAGCTTCAGCTTCAGCTTCAGCTTCAGCTTCAGCTTCAGCTTCAGCTTCAGCTTCAGCTTCAGCTTCAGCTTCAGCTTCAGCTTCAAGCTTCAGCTCAGCTCAGCTCAGCTTCAGCTTCAGCTTCAGCTTCAGCTTCAGCTTCAGCTTCAGCTTCAGC	4/6 CCTCHACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTT	

Query Match 88.8%; Score 1917; DB 6; Length 2092; Best Local Similarity 99.2%; Pred. No. 0; Matches 1940; Conservative 0; Mismatches 5; Indels 10; Gaps 1;	/oi/ /mc/ /di	Helix Research Institute (JP); Biotechnology (JP) Location/Qualifiers 1. 2092	hikawa,T., Otsuka,M., N	Sutheria; Primates; Catarri Sugiyama,T., Otsuki,T., Wa T Taono V. Hio V. Otsu	S Homo sapiens (human) ISM Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; I	AX/96/24 AX746724 2092 bp mRNA linear PAT 20-JUN-2003 DEFINITION Sequence 249 from Patent EP1308459. ACCESSION AX746724 CT.32130001	SULT 4	2096 GGTTTTGTAACTCATATGAAATAAAATCAGAATGTAAAATAGGAAAA 	Qy 2036 GGCAACAAGATTTCTTCAATAAATTTGGAAGAGGGCTGGCCTATTAGTTGTCATAATAAT 2095	Qy 1976 ACTTAGGAATGATCCTTACAGAATTCTTTTCAACATCAAAAAGTGGAATTTTGTCTTTGGAA 2035	Qy 1916 GCTCAGCTGCTTTCTATGGGGATCCTTGCAAAACAAGCTGCTTTCGCTGATATTTTATGG 1975	OY 1856 GTGATTTTGGTTTCCCTTCTCCTCCATAATTTCTCCCGCAATCATTAGCTTCTTTCT	Qy 1796 TTTCCTCTCCTCCTCCAGCCTTTCTTTTTCTTTTTGTGAGAAGTTATCTTTCT 1855	Oy 1736 CACCATCCCCTGATCCTGTCTGCCTCCGACATGCTCCACAGTCCTCTTTCTT	Qy 1676 GGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGGGGGTGGATTTTTTGGACCAG 1735	Qy 1616 TAATGGGAACGACCTGTCTCTGTGGCCAGCTTATAATCTGACTGA	Qy 1556 GAAGTTACTGAGCCGGAAGATGATGAATACTGGGCTACCTTTGCTCGAACCGGGAATCC 1615
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1196 CTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAGTA 1255	CAATAACCACGAGTGTGGCTTCCTGCTGCCTATGAAGGAGGCTCCTGAGATCCTCAGTGG	1076 TGAGCCTCTAGATCTATTGTCTCAGAAAGCATTTAAAGCAATTCCTTCC	1016 GACCCTCAGCCAGAAACAAAGTCTTTCACTCGAGTGGTTGATGGTGCTTTCTTT	956 TGCGTCAGACTCTGAGGCCCTGCTGAGGAGGACCAAAACCCTCCAAGGAGCTGCT 1015	GCCCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAA	836 CAAAGGCTTATTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGA 895	776 CATCTTTGGCGAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGC 835	716 TGCTCTGTCCTGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGGAC 775	TTTCTTCACCACATGGGATCAGCATGCTCCGGGAACTGGGCCTTCAAGGACCAGGTGGCTTCATGGATCAGGATCAGGATCAGGAACTGGGCCTTCAAGGACCAGGTGGC	CTTGGCTGCCTATGAGGACGTGCTGGTTGTGGTCCAGTACCGGCTAGGAATATTTGG CCTGGCTGCCTATGAGGACGTGCTGGTTGTGGTCCAGTACCGGCTAGGAATATTTTGG	GENERAL TO CHARGAGE TO CLI TO CH		GCTCTTAGATCAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTG				186 GGGCCTTCTGCTGAAGGGCCACAGAGGAACACCAGGCTGGGATGGAT

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Oligo capping; fis (full insert sequence).

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                    AK090997 2092 bp mRNA linear Homo sapiens cDNA FLJ33678 fis, clone BRAWH2002191, to FATTY ACYL-COA HYDROLASE PRECURSOR, MEDIUM CHAIN
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Wakamatsu, A. Hayashi, K. Sato, H. Nagai, K. Kimura, K. Makita, H. Sekine, M. Obayashi, K., Nashi, T. Shipajak, T. Tanaka, T. Ishi, S., Yamamoto, J. Saito, K. Kawai, Y. Isono, Y. Nakamura, Y. Shiraki, K. Murakami, K. Yasuda, T. Iwayanagi, T. Wagateuma, M. Shiratori, A. Sudo, H. Hosoiri, T. Kaku, Y. Kodaira, H. Kondo, H. Sugawara, M. Takahashi, M. Kanda, K., Yokoi, T. Furuya, T. Kikawa, E. Omura, Y. Abe, K. Kamihara, K. Kateuta, M. Sato, K. Tanikawa, K. Pujimori, K. Tanai, H. Kimata, K. Kateuta, M. Sato, K. Tanikawa, K. Pujimori, K. Tanai, H. Kimata, M. Watanabe, M. Hiraoka, S. Chiba, Y. Ishida, S. Ono, Y. Takiguchi, S. Watanabe, K. Yosida, M. Hotuta, T. Kusano, J. Kanehori, K. Takahashi Fuji, A. Yosida, M. Hotuta, T. Kusano, J. Kanehori, K. Takahashi Fuji, A. Takeuchi, K. Arita, M. Imose, N. Musashino, K. Yuuki, H. Oshina, A. Sasaki, N. Actsuka, S. Yoshikawa, Y. Metunawa, H. Ichihara, T. Shiohata, N. Sano, S. Moriya, S., Moniyama, H. Satoh, N. Takami, S. Goto, Y. Shimizu, F. Wakebe, H. Hishigaki, H. Watanabe, T. Suyiyama, A. Takemoto, M. Kawakami, B. Yamazaki, M. Watanabe, K. Kumagai, H. Tanagami, A., Fujiwara, T. Ono, T. Yamada, K. Fujii, Y. Ozaki, K. Hirao, M. Okomoti, Y. Kawabata, A. Hikiji, T. Kobatake, N. Nakajima, Y. Mizuno, T. Morinaga, M. Sasaki, M. Watanabe, K. Nagasei, T. Natanabe, M. Xatanabe, M. Nakajima, Y. Shirai, Y. Takahashi, Y. Nakagawa, K. Sanashin, T. Kobatake, N. Nakajima, Y. Kawakami, B. Yamazaki, M. Watanabe, K. Nakajima, Y. Kawakami, B. Yamazaki, M. Watanabe, K. Nakajima, Y. Kawakami, T. Kobatake, N. Nakajima, Y. Kawakami, T. Kawakami, T. Kobatake, N. Nakajima, Y. Kawakami, T. Kawakami, T. Shirai, Y. Takahashi, Y. Nakagawa, K. Okumura, K. Nakamura, Y. Nakagawa, K. Okumura, K. Nakamura, Y. Nakagawa, K. Okumura, K. Nakamura, Y. Nakagawa, K. Okumura, K. Nakamura, Y. Nakagawa, K. Okumura, K. Nakamura, Y. Ohara, O. Isogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length
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3 (bases I to 2092)
1 Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
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/translation="mlkvhypkfgvsedclyiniyapahadtgskipvivmfpggafk
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                                                                                                                                                                                                                                                                                                       394. .1803
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
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Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Wadan, A. Kodrigues, S.
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffbrd, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
AL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
CONA Library Preparation: Baylor Human Genome Sequencing (
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRBR Plate: 4 Row: e Column: 1.
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Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowie, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (29-APR-2004) National Institutes of Health, Mammalian Sene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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Homo sapiens hypothetical protein FLJ31547, mRNA (cDNA clone
MGC:97182 IMAGE:7262427), complete cds.
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1 (bases 1 to 2047)
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DB 9

Length 2047;

Matches 1855; 906 846 793 786 733 726 673 999 909 493 486 433 426 193 TATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAATGCGTCAGAC GAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTA 845 ACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCC TATGAGGACGTGCTGGTTGTGGTCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACC TTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGAGGCCCATGAT TGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGC ACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCC CCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCC 605 AACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTC TGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGC TATGAGGACGTGCTGGTTGTGGTCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACC AACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTC CAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTG CAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTG CGAGAAGCCACCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGAT CGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGAT cccccccracanteccancecanceccancecarcanceccaracateccaracana CCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG GTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCTTTGCTGCT GTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCCTTTGCTGCT 305 Conservative 86.0%; 0; Score 1855; Pred. No. 0; Mismatches 0; 0; Gaps 912 905 852 785 672 792 732 665 612 545 492 485 432 425 365 252 552 372 312

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Direct Submission
Submitted (01-NOV-2002) National Institutes of Health, Mammalian Submitted (01-NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 51 Row: k Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., I
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M.,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Baylor College of Medicine Human
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1 (bases 1 to 2298)
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nilarity 93.5%;
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/mol_type="mRNA"
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/clone="IMAGE:5174937"
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/lab_host="DH10B"
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ilarity 100.0%; Pred. No. 0;
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thereof
Patent: WO 0250256-A 3 27-JUN-2002;
Millennium Pharmaceuticals, Inc. (US)
                                                     Curtis,R.A. and Silos-Santiago,I. 53010, a novel human carboxylesterase
                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1116 ATTCCTTCCATCATCGAGTCAATAACCACGAGTGTGGCTTCCTGCTGCTGCTGAGGAGG 1175	1746; Qy s 0; Gaps 0; Db s 0; Gaps 0; Qy rGATTCTCCAGCCC 155	Match 80.9%; Score 1746; DB 6; Length 1746; ocal Similarity 100.0%; Pred. No. 0; 8 1746; Conservative 0; Mismatches 0; Indels 0; Gaps 96 ATGCCACAGGACTTACTTCATCTGCTTCACAATGGTGCTTTTTCCTGATTCTCAGCCC	Query Match Best Local s Matches 1746 Qy 96 Db 1
901 AAACCCTCCAAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACTCGAGTGGTT 960 1056 GATGGTGCTTTCCTTACTGAGCCTCTAGATCTATTGTCTCAGAAAGCATTTAAAGCA 1115	рь Оу оъ	Location/Qualifiers 1. 1746 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	FEATURES BOURG

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846 TICCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCTTACCTGGAGGCCCATGAT 905	726 TGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGC 785	642 TATGAGANCETGCTTGTTGTGTCGTCGTCCAGTACCGGCTAGGAATATTTTGTTTCATC /01 666 ACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTCTGTCC 725	CCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCCCTGCCTG	486 AACATCTATGCGCCTGCCCACGCCGATACAGGCTCCCAAGCTCCCCGTCTTGGTGTGGTTC 545	426 CAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTG 485	366 CGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGAT 425	306 CCCCCGCTGGGATTCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG 365	246 GTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCCTTTGCTGCT 305	SCCTTCTGCTGAAGGGCACAGAGGAACACCAGGCTGGGATGGAT	atch 73.2%; Score 1579.4; DB 6; Length 1962; cal Similarity 92.0%; Pred. No. 0; 1740; Conservative 0; Mismatches 1; Indels 150; Gaps 1;	ce 11962 /organism="Homo gapieng" /mol_type="unassigned DNA" /db_xref="taxon:9606"	Helix Resear Biotechnolog	Tamechika, I., Seki, N., Yo Masuho, Y. Full-Length CDNAs
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TITCTTCAATAAATTTGGAAGAGGGCTGGCC 1962	1692 CTCCTCCAGCCTTTCTTTCTTTTGTGCTCCTTGAGAAGTTATCTTTCTGTGATTTTGG 1751 1866 TTTCCCTTCCCCCATAATTTCTCCCGCAATCATTAGCTTCTTCTGAGCTCAGCTGC 1925	1746 CTGATCCTGTCTGCCTCCGACATGCTCCACAGTCCTCTTTCTT		1566 AGCCGGAAGATGATGAATACTGGGCTACCTTTGCTCGAACCGGGAATCCTAATGGGAAC 1625	GCTTCCTGAAGGGGACATTGTTATGTTCGAAGGAGCACGGAGGAGGAGGAGTTACTG	W. CATAMOR CANAL TATA TAMAMOR CANAL CANAL TAMAMOR CANAL TATA CANAL TATA CANAL TAMAMOR CANAL CANA		ACTIGCTIGGAGAIGTGTTCTITIGTGGTCCCTGCACTGAITCACAGCTCGAITATCACAGA	GTGGCTAATGAATACTTCCATGACAAGCACTCCCTGACTGA	1206 TCCCTTGCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAGTATTTGCACCTT 1265 	1146 GAGTGTGGCTTCCTGCTGCCTATGAAAGAAGGCTCCTGAGATCCTCAGTGGCTCCAACAAG 1205 	1086 GATCTATTGTCTCAGAAAGCATTTAAAGCAATTCCTTCCATCATCGAGTCAATAACCAC 1145	1026 CAGAAAACAAAGTCTTTCACTCGAGTGGTTGATGGTGCTTTCTTT

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DEFINITION
                                                                                                 Unpublished

3 (bases 1 to 1962)

3 (bases 1 to 1962)

8 Isogai, T., Otsuki, T. and Sugiyama, T.

18 Direct Submission

19 Direct Submission

10 Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan, CDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wakamateu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoco, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Koki, T., Furuya, T., Kikawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, M., Sato, K., Tanikawa, K., Pujimori, K., Tanai, H., Kimata, M., Watsuta, M., Sato, K., Yosida, M., Hotuta, T., Kusano, J., Kamchara, K., Katsuta, M., Sato, K., Yosida, M., Hotuta, T., Kusano, J., Kanchori, K., Takahashi-Pujii, A., Yosida, M., Hotuta, T., Kusano, J., Kanchori, K., Takahashi-Pujii, A., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, M., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shinhata, N., Sano, S., Moriya, S., Moniyama, H., Satoh, N., Takami, S., Goo, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sujiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, T., Sujiyama, A., Takema, Y., Makashata, N., Watanabe, T., Noguchi, S., Itoh, T., Kawakami, B., Yamazaki, M., Watanabe, K., Tasaina, Y., Mizuno, T., Watanabe, A., Hikiji, T., Kobatake, N., Nasajina, Y., Mizuno, T., Womatsu, T., Matanik, A., Kawakami, T., Matanik, T., Watanabe, T., Nakajina, Y., Mizuno, T., Womaza, M., Sasaki, M., Togashi, T., Nakajina, Y., Takahashi, Y., Nakajawa, K., Okumura, K., Nakamura, Y., Masuhoto, Y., Yamashita, R., Nakaina, Y., Matanabe, M., Takahashi, Y., Nakaniha, R., Nakaina, R., Kawakami, T., Nakaniha, R., Nakaina, R., Kawakami, T., Nakaniha, R., Nakaina, Y., Nakaniha, M., Takahashi, Y., Nakaniha, R., Nakaina, R., Nakaina, Y., Nakaniha, M., Takahashi, Y., Nakaniha, R., Nakaina, 
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                                                                             Evaluation; clone selection for full insert sequencing:
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oligo capping; fis (full insert sequence)
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Mammalia; Eutheria; Primates;
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                             Location/Qualifiers
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shi,K., Sato,H., Nagai,K., Kimura,K., Makita,H.,
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Best Local Sim
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GAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTA
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                                                                                                                                                                                                                                                                                                       TATGAGGACGTGCTGGTTGTGGTCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACC
                                                                                                    TGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGC
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CCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCC
TATGAGGACGTGCTGGTGTGGGCTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACC
                                       ccaegaegreccrrcaaeacregerecaecrerragerregerece
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ilarity 92.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="NT2RI2001010"
/cell_line="NT2"
/cell_type="teratocarcinoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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TITCCCTTCTCCCATAATTTCTCCCGCAATCATTAGCTTCTTTCT	CTCCTCCAGCCTTTCTTTTTCTTTTGTGCTCCTTGAGAAGTTATCTTTCTGTGATTTTGG	CTGATCCTGTCTGCCTCCGACATGCTCCACAGTCCTCTTTCTT	ATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTGGATTTTTGGACCAGCACCATCCCC	GACCTGTCTCTGTGGCCAGCTTATAATCTGACTGAGCAGTACCTCCAGCTGGACTTGAAC	AGCCGGAAGATGATGAATACTGGGCTACCTTTGCTCGAACCGGGAATCCTAATGGGAAC	GCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGAGGAAGTTACTG		ACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTTCGGTGGT		GATGCTGGTGCACCTGTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTGCTTTGAAGAC	GACTTGCTTGGAGATGTGTTCTTTGTGGTCCCTGCACTGATCACAGCTCGATATCACAGA	GTGGCTAATGAATACTTCCATGACAAGCACTCCCTGACTGA	TCCCTTGCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAGTATTTGCACCTT	GAGTGTGGCTTCCTGCTGCCTATGAAGGAGGCTCCTGAGATCCTCAGTGGCTCCAACAAG	GATCTATTGTCTCAGAAAGCATTTAAAGCAATTCCTTCCATCATCGGAGTCAATAACCAC	CAGAAAACAAAGTCTTTCACTCGAGTGGTTGATGGTGCTTTCTTT	TCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAACCCTCCAAGGAGCTGCTGACCCTCAGC	TATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAATGCGTCAGAC	TTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGAGGCCCATGAT	
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Clone distribution: MGC clone distribution information can be found

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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.B., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schbutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
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                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
cDNA Library Preparation: Baylor Human Genome Sequencing Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIMI)
DNA Sequencing by: Baylor College of Medicine Human Genome
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BC069548.1 GI:46854430
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (29-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                      Sequencing Center
Center code: BCM-HGSC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                          ACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCC
                                                                                                   TATGAGGACGTGCTGGTTGTGGTCCTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACC
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                        ACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCC
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IPSIIONNHECGFLLEMKEAPEILSGSNKSLALHLIQNILHIPPQVLHLVANEYFHD
KHSITEINGSLULIGDVFFVVPALITARYHREGATEEEKLLSRKMKKWATFAATGN
PNGNDLSLWPAXNLTEQYLQLDLNMSLGQRLKEPRVDFWTSTIPLILSASDMLHSPLS
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Location/Qualifiers
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/clone_Tib="NIH_MGC_244"
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g &	D Q	B &	용 성	Qy Db	р у	B &	Query Ma Best Loc Matches	ORIGIN	JOURNAL FEATURES	AUTHORS TITLE	ORGANISM	ACCESSION VERSION KEYWORDS	RESULT 13 CQ733044 LOCUS	B 5	S B 8	S B 6	S B
539 GTGGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCT 598	CTACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGT	419 CTTAGATCAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCT 478	359 TAACTTGCGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCT 418	299 TGCTGCTCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGA 358	239 CAAGCAAGTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCTT 298	179 AAAAACTGGGCCTTCTGCTGAAGGGCCACAGAGGAACACCAGGCTGGGATGGAT	/ Match 66.0%; Score 1425; DB 6; Length 1716; Local Similarity 99.7%; Pred. No. 0; nes 1428; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	/db/ /mc/ /oz/	L Patent: WO 02068579-A 18978 06-SEP-2002; PE Corporation (NY) (US) Location/Qualifiers 1 1716		M Homo Baplens (Abuman) SM Homo Baplens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	CQ733044 CQ733044.1 GI:42314969		42 GATCCTTACAGAATTCTTTTCAACATCAAAAAGTGCAATTTGTCTTGGAAGGCAA	8 8 6	722 TTTCCTTCTCCATAATTTCTCCCCCAATCATTAGCTTCTTTCT	11111111111111111111111111111111111111
RESULT 14 AX958392 LOCUS DEFINITION	D Q	D Q	₽ \$	}	}	p &	, B &	р, Q	da Q	B Q	B 8	B 8	B &	B 8	B &	B &	B 8
14 /2 AX958392 1857 bp DNA linear PAT 14-JAN-2004 TON Sequence 20 from Patent WO0226988.	1559 GTTACTGAGCCGGAACATGATCAAATACTGGGCTACCTTTGCTCGAACCGGGA 1611 	1499 CGGTGGTTCCTTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGAGGAGA 1558 	TGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTT 13	TCACAGAATACTGGTGCACCTGTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTGCTT TCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTGCTT TCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTTCGGCACCGGCCTCAGTGCTT TCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTTCGGCACCGGCCTCAGTGCTT TCACAGAGATGCTGGTGCACCTGTTTTTCGGCACCAGTGCTTT TCACAGAGATGCTGGTGTATGAGTTTTTTTTTT	TCTTCTGGACTTGCAGAAGTGTTCTTTGTGGTCCCTGCACTGACCACACTCGATA 137	GLACCTIGIGGUAIGATACTICCATGACACICCCTGACTGACACICCGACACACACICCCTIGACTGACACICCCAGACACACACICCCTTGTGGCTAATGATACTTCCATGACAAGCACTCCCTTGACTGAAATCCGAGACACAC	CAACAACTCCCTTGCCCTCCATCTGATACAAAAACATCCTGCCATCCCGCCTCAGTATTT	TAACCACGAGTGTGGCTTCCTGCTGCCTATGAAGGAGGCTCCTGAGATCCTCAGTGGCTC	1079 GCCTCTAGATCTATTGTCTCAGAAAGCATTTAAAGCAATTCCTTCC	1019 CCTCAGCCAGAAAACAAAGTCTTTCACTCGAGTGGTTGATGGTGCTTTCTTT	959 GTCAGACTCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAACCCTCCAAGGAGCTGCTGAC 1018 	899 CCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAATGC 958	839 AGGCTTATTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGAGGC 898	779 CTTTGGCGAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAA 838	719 TCTGTCCTGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCAT 778	659 CTTCACCACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGC 718	599 GGCTGCCTATGAGGACGTGCTGGTTGTGGTCCAGTACCGGCTAGGAATATTTGGTTT 658

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                            CAAAGGCTTATTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGA
                                                            AX958392
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                                                                                             h 64.2%;
Similarity 94.7%;
73; Conservative
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                            TTTCTTCACCACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGC
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/mol_type="unassigned DN
/db_xref="taxon:9606"
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       Miyazaki, M., Yamashita, T., cauxin family protein Published Only in Database 2 (bases 1 to 1728)
                                                                                       AB186392 1728 bp
Canis familiaris cauxin mRNA fo-
excreted protein, complete cds.
AB186392 GI:51014274
                                                                 Canis familiaris
Canis familiaris
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                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
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Yamashita, T.,
                                                                        (dog)
Taira, H.
                              Taira,H.
                (2004)
                                                                                                                for
                                                                                                             mRNA linear MAM 06-AUG-2004 carboxylesterase-like urinary
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and
Suzuki,
                               Suzuki, A.
                                                      Euteleostomi;
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Submitted (04-AUG-2004) Masao Miyazaki, RIKEN, Frontier System
Research, Supra-Biomolecular System Research Group; Hirosawa 2-1,
Wako-shi, Saitama 351-0198, Japan
(B-mail:mmiyazaki@postman.riken.jp, Tel:81-48-467-9619,
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                  ACAGGGGACCAGCACGCTCCGGGGAACTGGGCCTTCCTGGACCAGTTGGCTGCCTTAACC
                                                                                              TATGAGGATGTGCTGATTGTGACAACCCAGTACCGGCTAGGAATATTTGGTTTCTTCAAG
                                                                                                                   TATGAGGACGTGCTGGTTGTGGTCGTCCAGTACCGGCTAGGAATATTTTGGTTTTCTTCACC
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LPFLFSSAP"
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/mol_type="mRNA"
/db_xref="taxon:9615"
/chromosome="2"
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                                       CTGATAATGTCCATGTCCACAGCACCCCCTGGTCCTCCTGTCCCCTTACTCTCCCTTTCT
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Search completed: June 14, 2005, 22:52:42 Job time: 9387.39 secs

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Adc55523 Human car
Adf50146 Cat cauxi
Abg86171 Novel hum
Aad33344 Human car
Abz11273 Human pol
Adm43791 Novel hum
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Ada76491 Human PRO	Ada76547 Novel hum	Ada46060 Novel hum	Aca67707 cDNA enco	Aca04294 Human cDN	Aca68601 Novel hum	Human	Aca06084 cDNA enco	Abx89411 DNA encod	Aca03873 cDNA enco	Human	Abl95693 Human ang	Abl88204 Human PRO	Abk33640 cDNA enco	Aas21514 Human cDN	Aaa96341 cDNA enco	Human	Aad00680 Human Hyd	Abz24055 CES2 rela	Aaf21884 Human bre	Abn97359 Gene #385		Abl62492 Colon ade	Colon	Abz24051 CES2 rela	

ALIGNMENTS

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53010 nucleic acids, useful for diagnosing and treating e.g. vascular diseases, autoimmune diseases, or neurodegenerative diseases, as
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                                                                                                             WPI; 2002-547936/58.
P-PSDB; ABB79537.
                                                                                                                                                                                                                   Curtis RAJ, Silos-Santiago I;
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                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PHARM INC
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28-MAR-2001; 2001US-0279508P.
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174. .1838
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Matches 2158; Conserv
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tive 0; Mismatches
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3; 2003US-0445793DP.
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3; 2003US-0471614P.
3; 2003US-0478742P.
3; 2003US-0488529P.
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Use of polypeptides related to urological disorders, e.g. 44390, 5, 211 or for identifying a compound capable of treating a urological disorder or identifying and treating a subject having a urological
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P-PSDB; ADQ89094.
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Claim 1; SEQ ID NO 45; 542pp; English

The present invention describes the use of polypeptides related to urological disorders for identifying a compound capable of treating a urlogical disorder, identifying a subject having a urological disorder, or treating a subject having a urological disorder. Also described: (1) a method for identifying a compound capable of treating a urological disorder; (2) a method for identifying a subject having a urological disorder; and (3) a method for treating a subject having a urological disorder. The compound has uropathic and cytostatic activities. The polypeptides related to urological disorders are useful for identifying a compound capable of treating a urological disorder, identifying a urological disorder. Disorders include urinary incontinence and benign prostatic hyperplasia. The present sequence encodes a human urological disorder related protein, which is used in the exemplification of the present

Sequence 2158 BP; 515 A; 559 C; 509 ຸດ 575 T; 0 U; 0 Other;

2158

S 밁 문 ð 밁 밁 ঠ ð S S 밁 δ 5 밁 밁 밁 밁 ð 밁 δ Query Match
Best Local Similarity
Matches 2158; Conserv atch 100:0%; cal Similarity 100:0%; 2158; Conservative 0 541 541 481 481 421 421 361 361 301 301 241 241 181 181 121 121 61 61 CCACGCGTCCGAAAAACAGGCCTGGAGAGCAATGTGGGAGTAAGCAATGTAATAAAAACGA GGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGG TAGATCAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCT TAGATCAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCT ACTIGCGAGAAGCCACCICCTACCCTAATTIGIGCCTCCAGAACTCAGAGTGGCTGCTCT CTGCTCCCCCGCTGGGATCCCTGCGATTTACGAACCCCGCAGCCTGCATCGCCCTGGGATA CTGCTCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATA CCACGCGTCCGAAAAACAGGCCTGGAGAGCAATGTGGAGTAAGCAATGTAATAAAAACGA CTGCCTATGAGGACGTGCTGGTTGTGGTCGTCCAGTACCGGCTAGGAATATTTGGTTTCT GGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGG ACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGT ACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCCGTCTTGGTGT AGCAAGTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCCTTTG AGCAAGTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCTTTG 0; Score 2158; Pred. No. 0; 0; Mismatches 멂 13; <u>.</u> Indels Length 0, Gaps 360 360 600 420 240 180 600 540 540 480 480 420 300 300 240 120 120 60

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AAD40574 standard; cDNA; 2232 ВP

AAD40574;

30-OCT-2002 (first entry)

metabolising enzyme (DME-10) cDNA.

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XX Human; drug metabolising enzyme; autoimmune; inflammatory disorder; acquired immunedeficiency syndrome; AIDS; atherosclerosis; psoriasis; proliferative disorder; arteriosclerosis; cirrhosis; hepatitis; cancer; asthma; neurological disorder; Alzheimer's disease; Huntington's disease; dementia; Parkinson's disease; developmental disorder; namemia; adenoma; drug screening; endocrine disorder; conjunctivitis; glaucoma; cataract; renal tubular acidosis; eye disorder; epilepsy; thrombosis; peptic ulcer; anorexia; metabolic disorder; cystic fibrosis; diabetes; liver disorder; goitre; gastrointestinal disorder; gene therapy; virucide; anticoagulant; nootropic; enzyme; DMS-10; gene; ss.

Homo sapiens.

음 성 음

S 음 성

밁 중 유 S 밁 δ 밁 Ś 밁 5 밁 중 유

mat_peptide sig_peptide /*tag= a /product= 1. .150 /*tag= b 151. .1926 /*tag= c /product= Location/Qualifiers "Mature "Human DME-10" human DME-10"

WO200246426-A2

04-DEC-2001; 2001WO-US047429

13-JUN-2002

08-DEC-2000; 2000US-0254308P. 15-DEC-2000; 2000US-0256189P. 21-DEC-2000; 2000US-0257713P.

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743 655

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CC are selected from autoimmune/infilammatory disorder such as acquired CC immunodeficiency syndrome (AIDS), asthma, atheroselerosis, psoriasis, CC uveitis; a dell proliferative disorder such as arteriosclerosis, CC cirrhosis, hepatitis, and cancer; a neurological disorder such as CC Alrheimer's disease, Huntington's disease, dementia, Parkinson's disease; CC adevelopmental disorder such as renal tubular acidosis, epilepsy, CC anaemia; an endocrine disorder such as adenoma, thrombosis and infections CC disorder such as conjunctivitis, glaucoma, cataract; metabolic CC disorder such as conjunctivitis, glaucoma, cataract; metabolic CC disorder such as cystic fibrosis, diabetes and goitre; a gastrointestinal CC useful in a number of drug screening techniques and to analyse the CC useful in a number of drug screening techniques and to analyse the CC useful in a number of cell type. The invention is useful for creating CC throck-in humanised animals or transgenic animals to model human diseases, CC in somatic or germline gene therapy, to generate a transcript image of a CC tissue or cell type, for detecting differences in the chromosomal CC disorder in to to transgenic animals to model human diseases, CC in somatic or germline services on the chromosomal CC disorder in the chromosomal corrier or affected individuals, and as hybridisation probes for mapping naturally occurring genomic sequences. The present sequence is human DME-10 cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human drug metabolizing polypeptide, useful in diagnosis, prevention or treatment of autoimmune/inflammatory, cell proliferative, peurological, developmental, endocrine, metabolic and gastrointestinal
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Lee EA, Ding L, Ha
Lal PG, Warren BA,
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, Hafalia AJA, Tang YT, Yue H, T
BA, Yang J, Walia NK, Nguyen DB,
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8 뫄 5 문 중 유

S 문 ર્ક 뮍 ð 문

New diagnostic and therapeutic polynuclectides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.

Claim 1; Page; 190pp; English

The invention relates to novel diagnostic and therapeutic polynucleotides CC selected from one of the 2722 sequences defined in the specification. A CC polynucleotide of the invention may have a use in gene therapy. The human CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be CC used to diagnose a particular condition, disease or disorder associated CC with human molecules, e.g. cell proliferative disorders, which the provider disorders associated CC utoimmune/inflammatory disorders, gastrointestinal disorders, or CC infections caused by virus, bacteria, fungi or parasite. The dithp CC molecules may also be used in genetic mapping, in identifying individuals CC from minute biological samples, in detecting single nucleotide constitutes as molecular weight markers, and for somatic or germline CC gene therapy. The present sequence represents a dithp polynucleotide of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format CC directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm

Sequence 2229 BP; 503 A; 585 C; 547 G; 594 T; 0 U; 0 Other;

Matches 1955; Query Match Best Local

Similarity

89.8%;

Score 1937.4; Pred. No. 0; 0; Mismatches

DB 13; Length

Conservative

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Isogai T, Su 05-NOV-2001; 2001JP-00379298. 25-JAN-2002; 2002US-00350978. (REAS-) (-ITEH) HELIX RES INST.
RES ASSOC BIOTECHNOLOGY. , Sugiyama T, J, Isono Y, Yoshikawa T, Otsuki T, Wakamatsu A, Sato H, I, Hio Y, Otsuka K, Nagai K, Irie R, Otsuka M, Nagahari K, Masuho Y;

Ishii S;

New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. P-PSDB; WPI; 2003-450961/43. DB; ADB64065. Tamechika ŗ,

Claim 1; Page; 222pp; English.

therapy.

The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide of the polynucleotide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide

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20-DEC-2000;
09-JAN-2001;
30-JAN-2001;
            The invention relates to an isolated polypeptide with signal sequences which allow it to be secreted extracellularly or membrane associated. 'activity of polypeptides of the invention may be described as, cytostatic, vulnerary, antiarterisclerotic, antiparkingonian, nootrop.
                                                                                                                                                           Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder
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Martensen SA,
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Best Local Similarity
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Pred. No. 0;
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14-SEP-2001;
24-JAN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2002; 2002EP-00006586
polynucleotides encoding full-length polypeptides, e.g. secretory
/or membrane proteins, useful for developing medicines for diseases
ch the gene is involved, or as target molecules for gene therapy.
                                                                                                 2003-395539/38.
DB; ADA54807.
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O J, Isono Y, I
Yoshikawa T,
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2002US-0350435P.
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BIOTECHNOLOGY.
                                                                                                                                                              Otsuki T, Wakamatsu A, Sato H,
Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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Tamechika
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Claim 1; SEQ ID NO 736; 205pp; English.

The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease. Sequence 1962 BP; 428 A; 541 C; 473 G; 520 T; 0 U; 0 Other

В

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Similarity
TATGAGGACGTGCTGGTTGTGGTCGTCCAGTACCGGCTAGGAATATTTTGGTTTCTTCACC
                                            CCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCC
                                                                                                        CAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTG
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Pred. No. 0;
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ABX72267 standard; CDNA; 1746 ₽₽

03-JUN-2003 (first entry)

#98

Human; NOVX; gene; ss; metabolic disorder; cardiomyopathy; diabetes; ASD; hypertension; congenital heart defect; actric stenosis; valve disease; atrial septal defect; atrioventricular canal defect; ductus arteriosus; pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD; tuberous sclerosis; scleroderma; atherosclerosis; infectious disease; obesity; anorexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoletic disorder; haemophilia; hypercoagulation; Crohn's disease; cancer.

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WO200281498-A2

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03-APR-2002; 2001US-0281086P.
2001US-0281136P.
2001US-0281863P.
2001US-0281906P.
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Best Local (
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19-JUN-2001;

12-SEP-2001;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guo X, Kekuda R, Miller CE, Malyankar UM, Spytek KA; Patturajan M, Liu X, Gusev VY, Li L, Vernet CAM, Zerhusen BD Gorman L, Shenoy SG, Pena CEA, Smithson G, Burgess CE, Gerla Padigaru M, Shimkets RA, Gangolli EA, Taupier RJ, Casman SJ; Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ; Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA;
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20-DEC-2000; 2000US-0257048P.
09-JAN-2001; 2001US-02660482P.
30-JAN-2001; 2001US-0264922P.
06-FEB-2001; 2001US-0266797P.
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                                                        Agarwal P, B:
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cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic, corporatective, immunosuppressive, haemostatic, antiinflammatory, cardiant, antiulcer, virucide, antithyroid, cerebroprotective, anorectic, and metabolic. Polypeptides and polynucleotides of the invention are useful in the treatment, or as a vaccine in the prevention of, cancer, wound healing disorders, infection, attherosclerosis, Parkinson's disease and Alzheimer's disease, autoimmune disorder, haematopoietic disorder, inflammation, neoplastic diseases, nervous system related disorders and cardiovascular disorders, pancreatitis, respiratory disorder, inflammation, systemic autoimmune disease, hyper-immunity, developmental abnormality, gastrointestinal ulceration, neuropathy, developmental diseases, metrodiseases, sperm dysfunction, thyroid disorders e.g. hypothyroidism, brain damages, colitis, cone phototuralition deficiency, neurological diseases, stroke, angiogenesis, trachea, thymus, lymph node and muscular system, obesity, anorexia, provides and alleviation of precoclous puberty. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated polypeptide with signal sequences which allow it to be secreted extracellularly or membrane associated. I activity of polypeptides of the invention may be described as, cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2(a); Page 251-252; 335pp; English.
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Sequence 1746 BP; 401 A; 464 C; 459 G; 422 T; 0 U; 0 Other;

sequences given in records ABQ86130-ABQ86184 represent novel human cDNA's of the invention

5 밁 S 밁 S 밁 S 밁 ঠ 맑 S 맑 δ 밁 ð 밁 S Query Match Best Local Simi Matches 1494; 493 909 433 546 373 313 426 193 486 253 366 306 133 246 73 Similarity ACATGGGATCAGCATGCTCCGGGGAAACTGGGCCTTCCAAGGACCAGGTGGCTGCTCTGTCC TATGAGGACGTGCTTGTTGTGGTCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACC CCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCC CAACATATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTG CAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTG CGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGAT CCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG CCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG GTCACTGTGCTGGGAAGCCCTGTGCACGTGTTCCTCGGAGTCCCCTTTGCTGCT GTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCCTTTGCTGCT CCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCC AACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTC AACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTC CGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTAGAT Conservative 95.4%; 0; Mismatches Score 1432.4; Pred. No. 0; BB 51; 6, Indels 21; Length 1746 Gaps 725 552 665 492 605 432 372 485 312 425 252 365 192 305 132

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Azimzai Y, Baughin MR, Bo
Elliott VS, Gandhi AR, Ga
Lal P, Lee EA, Lu DAM, N
Ring HZ, Sanjanwala MS, J
Walsh RT, Warren BA, Xu )
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06-OCT-2000;
20-OCT-2000;
09-NOV-2000;
16-NOV-2000;
22-NOV-2000;
30-NOV-2000;
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; 2000US-0238664P.
; 2000US-0242323P.
; 2000US-0247581P.
; 2000US-02475919.
; 2000US-0252834P.
; 2000US-0252837P.
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Griffin JA, Hafalla AJA, Ison CH,
Nguyen DB, Arvizu C, Policky JL,
Tang YT, Tribouley CM, Narinder W
U Y, Yang J, Yao MG, Yue H;
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유정

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2002-362498/39. DB; ADR19663.

Human drug metabolizing enzymes, useful in the diagnosis and treatment disorders associated with aberrant (DME) activity, e.g., cancer and autoimmune disorders. of.

Claim 12; SEQ ID NO 20; 142pp; English.

This invention relates to novel drug metabolising enzymes (DME) and the nucleotide sequences which encode them. The invention may be useful for the development of compounds with a cytostatic, immunosuppressive, antiinflammatory, endocrine, ophthalmological, gastrointestinal or hepatotropic activity acting as an agonist or antagonist of drug metabolising enzyme activity. The invention may be used in the diagnosis and treatment of disorders associated with decreased or increased expression or activity of drug metabolising enzymes. Such disorders expression or activity of drug metabolising enzymes. Such disorders include cancer, cell proliferative disorders, autoimmune/inflammatory, endocrine, eye, gastrointestinal (including liver disorders) and metabolic disorders. The present sequence is that of a gene which encodes a human drug metabolising enzyme (DME) of the invention. Note: This sequence did not form part of the printed specification but was obtained in electronic format from EPO.

Sequence B₽; 428 A; 487 C; 496 <u>ი</u> 446 T; 0 Ģ 0 Other;

Query Match

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P-PSDB; ADC55524.
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Polypeptide-human carboxylatase-24.64 and polynucleotide for coding it.
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XX I 09-SEP-2003. Cat cauxin encoding JP2003250575-A. ADF50146 12-FEB-2004 cauxin; standard; cDNA; cat kidney disease marker; (first CDNA SEQ entry) 2145 ID NO:3. ₽₽ kidney disease; gene;

04-MAR-2002; 2002JP-00057908

(TOHO-) TOHOKU TECHNOARCH

04-MAR-2002; 2002JP-00057908

2004-002277/01. DB; ADF50147.

Novel ca cauxin protein or its salt, useful as or diagnosing cat kidney disease. þ cat kidney disease marker,

Claim 6; SEQ ID NO 3; 33pp; Japanese.

The present sequence encodes a cat cauxin protein (I) or its salt, which is cat kidney disease marker. Also described: (1) a partial peptide (II) of (I); (2) a nucleic acid (III) encoding (I) or (II); (3) a vector (IV) comprising (III); (4) a transformed host (V) comprising (III) or (IV); (5) producing (I) or (II) by culturing (V); (6) a antibody (IV) which couples specifically with (I) or (II); (7) diagnosing cat kidney disease which involves measuring (I) quantitatively, and where reduction of amount of (I) indicates presence of the disease; (8) a cat kidney disease diagnostic agent comprising (I) labelling agent, a reagent which measures the biological activity of urinary (I) or (VI); and (9) a cauxin and the biological activity of urinary (I) or (VI); and (9) a cauxin and the biological activity of urinary (I) or (VI); and (9) a cauxin cat kidney disease marker and (VI) is useful for disgnosing cat kidney disease. (I) enables detection of cat kidney disease simply and correctly. (I) provides an early marker for the disease, and replaces

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Query Match 53.6%; Score 1156; DB 12; Length 2145; Best Local Similarity 78.2%; Pred. No. 2.1e-285; Matches 1466; Conservative 0; Mismatches 386; Indels 22;
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Best Local Similarity
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                                                         CTGAGCAGGAAGATGAGGTACTGGGCCAACTTTGCTCGGACCGGGGACCCTAACGGG
                                                                            CTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACCGGGAATCCTAATGGG
                                                                                                                                          GGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGAGAAGTTA 1562
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                                                                                                                        GGTGCCTTCCTGAAAGGCGACATTGTCATGTTCGAAGGAGCCACCGAGGAGGAGAAATTG
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                                                                                                                                                                                                                                                                                       20-DEC-2000;
09-JAN-2001;
30-JAN-2001;
                                                                     Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder
                                                                                                                                                                                                                                                     19-MAR-2001;
04-APR-2001;
The invention relates to an isolated polypeptide with signal sequences which allow it to be secreted extracellularly or membrane associated. 'activity of polypeptides of the invention may be described as,
                                                                                                                                                                                          (SMIK)
                                                                                                                                                                                                                                                                            06-FEB-2001;
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                                                                                                                                                         Martensen SA,
                                                                                                                                                                   Agarwal P,
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                                                                                                                                 2002-508784/54.
                                               2(a); Page 252; 335pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                abnormality; precocious puberty; gene; ss.
                                                                                                                      ABP61006.
                                                                                                                                                                                         SMITHKLINE BEECHAM
SMITHKLINE BEECHAM
GLAXO GROUP LTD.
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2001US-0264922P.
2001US-0266797P.
2001US-0276988P.
2001US-0276988P.
2001US-0281535P.
2001US-0289622P.
                                                                                                                                                        Birkeland M,
A, Rizvi SK,
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Smith RF, Strum JC, Xie Q;
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ce neuroprotective, immunosuppressive, haemostatic, antinflamatory, cardiant, antiulcer, virucide, antithyroid, cerebroprotective, anorectic, and metabolic. Polypeptides and polynucleotides of the invention are cuseful in the treatment, or as a vaccine in the prevention of, cancer. CC wound healing disorders, infection, atherosclerosis, Parkinson's disease and Alzheimer's disease, autoimmune disorder haematopoietic disorder, inflammation, neoplastic diseases, nervous system related disorders and cardiovascular disorders, pancreatitis, respiratory disorder, cc haematopoietical disorders and cardiovascular disorders, pancreatitis, respiratory disorder, cc developmental abnormality, gastrointestinal ulceration, neuropathy, cc developmental abnormality, gastrointestinal ulceration, thyroid disorders e.g. hypothyroidism, brain damages, sperm dysfunction, thyroid clisorders e.g. hypothyroidism, brain damages, colitis, cone photoctransduction disorders, diseases in the spinal cord, thyroid gland, heart, cc cyclation disorders, diseases in the spinal cord, thyroid gland, heart, cc growth abnormalities, and alleviation of precocious puberty. The cc sequences given in records ABQ86130-ABQ86184 represent novel human cDNA's of the invention
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Sequence 1071 BP; 242 A; 286 C; 254 G; 289 T; 0 U; 0 Other;

47.3%;

Score 1021.4; DB 6; Pred. No. 4.8e-251;

Length

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Query Match
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Matches 1022; Conserv
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                    GATGAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGGACATTGTTATGTTCGAA
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GATGAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAA
                                                                    CGGCACCGGCCTCAGTGCTTTGAAGACACGAAGCCAGCTTT
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                                                             Novel human carboxylesterase-like enzyme polypeptide, regulators of which are useful for preventing and treating organophosphorus intoxication, cancer and osteoporosis.
 The invention relates to a purified human carboxylesterase-like enzyme polypeptide. Carboxylesterase-like enzyme and its DNA are useful for screening for agents which decrease or modulate the activity of carboxylesterase-like enzyme polypeptide. Carboxylesterase-like enzyme
                                               Claim 1;
                                                                                                      P-PSDB;
                                                                                                              WPI; 2002-195808/25
                                                                                                                                                                    17-JUL-2000;
                                                                                                                                                                                                                                                                                                         Human; carboxylesterase-like enzyme; organophosphorus intoxication; gen osteopathic; gene therapy; osteoporosis; antisense therapy; cytostatic; detoxifying agent; Paget's disease; bone implant degradation; cancer; dental implant; enzyme; gene expression; ss.
                                                                                                                                                                                     10-JUL-2001; 2001WO-EP007919
                                                                                                                                                                                                                          WO200206454-A2
                                                                                                                                                                                                                                                                                                                                                      Human carboxylesterase-like enzyme cDNA.
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CC disease, such as organophosphorus intoxication, cancer and osteoporosis.
CC compounds that increase the ability of human carboxylesterase-like enzyme
CC compounds that increase the ability of human carboxylesterase-like enzyme
CC control to organophosphorus compounds are useful as detoxifying agents.
CC carboxylesterase-like enzyme agonists and antagonists are useful for
CC treating osteoporosis, Paget's disease and degradation of bone implants,
CC particularly dental implants. Carboxylesterase-like enzyme is useful in
CC diagnostic assays for detecting diseases and abnormalities or
CC susceptibility to disease or abnormalities related to the presence of
CC mutations in the nucleic acid sequences which encode the enzyme. The
CC coding sequence of carboxylesterase-like enzyme polynucleotide is useful
CC in gene therapy and for generating antisense oligonucleotides or
CC carboxylesterase-like enzyme DNA. These antisense oligonucleotides are
CC useful for modulating carboxylesterase-like enzyme gene expression. The
CC useful for modulating carboxylesterase-like enzyme gene expression. The
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Best Local Similarity
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0; Mismatches 49;
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Search Job ti	ďa	Ş	В	Ş	망
Search completed: June 14, 2005, 18:10:04 Job time : 1175.6 secs	827 CAGCTCAGTATCATAGAGGTG 847	1369 CAGCTCGATATCACAGAGATG 1389	767 TCCGAGACAGTCTTCTGGACTTGCTTGGAGGATGTGTTCTTTGTGATCCCTAAGCTGATCA 826	1309 TCCGAGACAGTCTTCTGGACTTGGAGATGTGTTCTTTGTGGGTCCCTGCACTGATCA 1368	707 CCAATTATTTGCACCTTGTGGCTGGTGAATACTTCCATGACAAGCACTCCCTGACTGA

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Maximum Match 100%
Listing first 45 summaries
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match Length DB
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Copyright (c) 1993 - 2005 Compugen Ltd.
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ALIGNMENTS

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AY414461
AY414461.1 GI:39770423
GSS.
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                                                                                                                              2 (bases 1 to 1680)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306
                                                                     Submitted (16-NOV-2003) Celera Genom. Rockville, MD 20850, USA This sequence was made by sequencing them based on alignment.
                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1680)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
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Science 302 (5652), 1960-1963
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ilarity 100.0%;
Conservative 0
   /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
                                               1. .1680
                                                        Location/Qualifiers
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Pred. No. 9.1e-119;
0; Mismatches 0;
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                  TTTAAAGCAATTCCTTCCATCATCGGAGTCAATAACCACGAGTGTGGCTTCCTGCTGCCT 1166
                                                            GGTGTGGTGGAGAGTTCCTACCCAAGCATCCTC
                                                                          CGAGTGGTTGATGGTGCTTTCCTTACTAATGAGCCTCTAGATCTATTGTCTCAGAAAGCA 1106
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                                                                                                                                                                                         CAGGTGGTTGCACATTTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCTGCTGAGGTGC
TTTCACCCTGTCCCCAGCATCATTGGTTTCAACAATGATGAGTATGGTTGGATCGTCCCC
                                                                                                                                          AGTGGGGTGGCCTGCCTTACCTTATCTCCAACACCTCTGAGA-----TGGTCTCC
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/gene="CES2"
/locus_tag="HCM5231"
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Pred. No. 3.5e-102;
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                                                                                     CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.B. Consortium/LLNL at:
http://imagge.lnl.gov
Plate: LLAM11435 row: 1 column: 10
                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                       National Institutes of Health, Mammalian Unpublished (1999)
                                                                                                                                                                                                                                                                    1 (bases 1 to 576)
NIH-MGC http://mgc.nci.nih.gov/.
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GTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCTTATGCTGC GCGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTAGA 424 CCTATGAGGACGTGCTGGTTGTGGTCGTCCAGTACCGGCTAGGAATATTTTGGT 656 TGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCCAAGCTCCCCGTCTTGGTGTGT 543 TCCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTT GTCACTGTGCTGGGAAGCCCTGTGCACCGTGTTCCTCGGAGTCCCCCTT-TGCTGC 304 TCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTG TCAACACATGCTCAAGGTGCATTACCCGAAATTCGG-AGTGTCAGAAGACTGCCTCTACC GCGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGA TCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTT Score 414.6; DB 4; Pred. No. 3e-101; 0; Mismatches 14; - crecarerrigaregerececerec DB 4; Length Indels 576; ω •• 163 603 483 343 283 364 223 245 403

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 435)
Liang, G., Miao, S.Y., Zhang, X.D., Wang, L.J. and Wang, L.F.
The differentially expressed gene in spermatogenensis
Unpublished (2002)
Contact: Lin-Fang Wang
National Laboratory of Medical Molecular Biology
Institute of Basic Medical Sciences; Chinese Academy of Medical
Sciences & Peking Union Medical College; Chinese National Human BM422399 435 bp mRNA linear EST 01 HAS05_70 Human testis cDNA library Homo sapiens cDNA, mRNA Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. EST 01-FEB-2003

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genomic survey sequence.
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AY414459.1 GI:39770421
GSS.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1680)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous
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Homo sapiens
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#5, Dong Dan 3 Tiao, Beijing 100176, p.
YongChang Road BDA, Beijing 100176, p.
Tel: 8610-65296418
Fax: 8610-65240529
Email: wanglf@cdm.imicams.ac.cn.
Location/Qualifiers
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/dev_stage="adult"
/dev_stage="Human testis cDNA library"
/clone_lib="Human testis cDNA library"
/note="The cells of Primary Spermatocyte and Round
Spermatid were isolated from Human testis. Total RNA was
extracted by TRIzol. Using PCR-Select cDNA Subtraction
Kit, the library was constructed"
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|mol_type="mRNA"
|db_xref="taxon:9606"
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Pred. No. 3.7e-99;
0; Mismatches 2
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VIRTUAL
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P.R.China
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Submitted (16-NOV-2003) Celera Genomics,
Rockville, MD 20850, USA
GTGGCGTGGCCTCCTGCCCGGCCTCATTGCCAGCTCAGCTGA----
                    GTGGGGTGGCCATCATCCCTTACCTGGAGGCCCATGATTATGAGAAGAGTGAGGACCTGC
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Location/Qualifiers
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                                                                                                        ACTTTGGAGGCAACCCTGACCGTGTCACCATTTTTGGCGAGTCTGCGGGTGGCACGAGTG
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                                                   TGTCTTCGCTTGTTGTGTCCCCCATATCCCAAGGACTCTTCCACGGAGCCATCATGGAGA
                                                                     TTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTATTCCACAAAGCCATCATGGAGA 867
                                                                                                                            TCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGCGAGTCCGCGGGAGCCATAAGTG
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|mol_type="genomic DNA"
|db_xref="taxon:9606"
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/gene="CES2"
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                                                                                                                                                                                                                       Mus musculus adult male colon CDNA, RIKEN full-length enriched library, clone:9030624L02 product:similar to CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (AL PRODUCT STERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAINE ESTERASE) (PROCAINE ESTERASE) (METHYLBUTYRASE)
[Mesocricetus auratus], full insert sequence.
Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                Mus musculus
                                                                                              HTC; CAP trapper.
Mus musculus (house mouse)
                                                                                                                                                           AK033563.1 GI:26329244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc:riken.jp, UKL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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Please visit our web site for further URL:http://genome.gsc.riken.jp/
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Genomic Sciences Center and Genome Science Laboratory in R
Division of Experimental Animal Research in Riken contribu
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Analysis of the mouse transcriptome of 60,770 full-length CDNAs
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                                 organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
   db_xref="FANTOM_DB:9030624L02"
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                         TTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGCGAGTCCGCGGGAGCCATAAGT
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/db_xref="GI:26329245"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2687)
                                                                              Submitted (16-ARR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoham Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Pax.81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group
Genomic Sciences Center and Genome Science Laboratory in F
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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(ALI-ESTERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAINE ESTERASE)
(PROCAINE ESTERASE) (METHYLBUTYRASE) [Mesocricetus auratus],
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Please visit our web site for further details.
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LVHVKDTDIAVHTFLGIFFAKFPVGEVEFAFPAFPEAFBFWGVRDGTSHPWCLQKUNLM
GSEDLKMMKLLIPFISMSEDCLYLNIYVPAHAHEGSNLPWMWIHGGALTVCGMASWD
GSMLAATEDVVVVAIQYRLGVLGFFSTGDQHAKGNWGYLDQVAALRWVQQNIVHFGGN
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/db_xref="GI:26346112"
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/mol_type="mRNA"
/strain="C57BL/6J"
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Adachi.J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Takaku, Akahira, S., Takasu, M., Takahashi, F., Takaku, Akahira, S., Muzamatsu, M., and Hayashizaki, Y., Tayama, A., Takahashi, F., Takaku, Akahira, S., Muzamatsu, M., and Hayashizaki, Y., Tayanishi, A., Muzamatsu, M., and Hayashizaki, Y., Yasunishi, A., Muzamatsu, M., and Hayashizaki, Y., Tayamishi, A.,
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The RIKEN Genome Exploration Research Group FANTOM Consortium
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Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A43008BEI2 product:similar to CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ALI-ESTERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAINE ESTERASE) (PROCAINE ESTERASE) (METHYLBUTYRASE) (Mesocricetus auratus), full insert sequence.
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Mammalia; Eutheria; Rodentia;
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CDNA library was prepared and sequenced in Mouse Genome Exploration Research Group in Rignoyclopedia Project of Genome Exploration Research Group in Rignomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed prepare mouse tissues.

Please visit our web site for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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CTGCCTATGAGGACGTGCTGGTTGTGGGTCCAGTACCGGCTAGGAATATTTTGGTTTCT
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/clone Iib="RIKEN full-length enriched mouse
/dev_stage="0 day neonate"
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                     Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

AL Nature 420, 563-573 (2002)

CE 6 (bases 1 to 1958)

RS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Kouda, M., Koya, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohasto, N., Sano, H., Saeaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tanaka, T., Tomaru, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M., and Hayashizaki, Y., Takahashi, F., Takaku-Akahira, S., Niracri Shibata, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A.,
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Submitted (16-APR-2002) Yoshihide Hayashizaki,
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                                                                                                                                                                                                                                                                                                                                                                                              The FANTOM Consortium and the
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130231C15 product:similar to LIVER CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) [Mesocricetus auratus], full insert
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Please visit our web site for further details.

URL:http://fantom.gsc.riken.jp/.

URL:http://fantom.gsc.riken.jp/.
    CCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCCACGCC
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ilarity 55.1%;
Conservative
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Pred. No. 1.3e-92;
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Physical and Chemical Research (RIKEN), Laboratory for Gen Exploration Research Group, RIKEN Genomic Sciences Center RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216) Genome Yokohama,

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rigenomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to in Riken contributed to

/tlssue_type="cecum" /clone_Tib="RIKEN_full-length_enriched_mouse /dev_stage="adult" 56__1740 cDNA library"

/note="unnamed protein product; putative similar to LIVER CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) [Mesocricetus auratus] (SWISSPROT|Q64419, evidence: FASTY, 78.4%ID, 100%length, match=1674)"

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VLDHDEQYLQLDTQPAVGRALKARRLQFWTKTLPQKIQELKGSQDKHAEL"

Length 1958;

270 ccieleaveceleiliciceeveticectilieciectecececeeveticectece GGTGTCCATGCCTTCCTGGGAATCCCCTTTGCCAAGCCTCCTGTAGGACTACTGCGCTTT TTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGATCAACACATGCTCAAGGTGCATTAC GCACCTCCTGAGGACCCTGAGCCATGGAGTGGTGAGAGATGGGACCTCACAGCCGGCC ACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTGCGAGAAGCCACCTCCTACCCTAAT ATGTGTCTGCAGCCTGATATAATGAATTTAGAGGATGCGAAGGAAATGAATCTGATCCTG AGGAACACCAGGCTGGGATGGATTCAGGGCAAGCCAAGTCACTGTGCTGGGGAAGCCCCTGTG AGGAĀCĀĊĊCACAGĠĠĠTCAĠGTGAGAĠĠĊĀGCTTTĞTĊCACĠTĠAAĠĠACĀCTAAATCT 509 449 404 284 224 269

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                                                                                                    TTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAG
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                                                                                                                                                                                                                                                                                                                                    Punctional annotation of a full-length mouse Nature 409, 685-690 (2001)
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Please visit our web site for further details.

URL:http://fantom.gsc.riken.jp/.

URL:http://fantom.gsc.riken.jp/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Institute; (E-mail:genome-res@gsc.riken.jp, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
                  GTGCCTCCAGAACTC-----AGAGTGGCTGCTCTTAGATCAACACATGCTCAAGGTGCA
                                                                              GAACCCGCAGCCTGCATCGCCCTGGGATAACTTGCGAGAAGCCACCTCCTAACCCTAATTT
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                                                      TCCACCACAGCCTGCAGAGCCCTGGAGCTTCGTGAAGAACACCACCTCCTACCCGCCTAT
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Direct Submission
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1944
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/db_xref="GI:26347581"
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/dev_stage="adult"
64. .1761
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/clone="9030604P03"
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/strain="C57BL/6J"
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                                                                                                                          TGACCTCACCAAAAAGAAAGACCTGTTCCAGGACTTGATGGCTGATGTGGTATTTTGGTGT
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKPZ), Email s.wlemann@dkfz-heidelberg.de; sequenced by DKPZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZ)434N0935) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi*CloneID=DKFZp434N0935 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
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Homo sapiens mRNA; cDNA DKFZp434N0935 (from clone DKFZp434N0935).
AL713761.
AL713761.1 GI:19584506
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Submitted (22-SEP-2004) MIPS,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone_Tib="434 (synonym: htes3). Vector pSport1; host
DH10B; sites NotI + SalI"
/product="hypothetical protein"
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                                                                                                                  'gene="DKFZp434N0935"
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                   TGCGGGGCAAGAGTAAAGAGGAGATTCTTGCAATTAACAAGCCTTTCAAGATGATCCCCG
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GQVLGSLVHVKGANAGVQTFLGIPFAKPPLGPLRFAPPEBPBSWSGVRDGTTHPAMCL
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MASLYDGSMLAALENVVVVIIQYRLGVLGFFSTDCHATGNMGYLDQVAALRMVVQNI
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SADFQPVPSIVGVNNNNEFGMLIPKVNRIYDTGKSMDREASQAALQKMLTLLMLPPTFG
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1246 GGACCACACACACGGGCAGGTGCTGGGGAGTCTTGTCCATGTGAAGGGCGCCAATGCCG 1305 211 дарасассавествеватеваттся веселя всем втем стете стете стете с Similarity TTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTATTCCACAAAGCCATCATGGAGA **ACTITIGGAGGCAACCCTGACCGTGTCACCATTTTTTGGCGAGTCTGCGGGTGGCACGAGTG** GCAACTGGGGCTACCTGGACCAAGTGGCTGCACTACGCTGGGTCCAGCAGAATATCGCCC 1785 GGAACTGGGCCTTCAAGGACCAGGTGGCTGGCTGCTGTCCTGGGTCCAGAAGAACATCGAGT 747 TCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACCACATGGGATCAGCATGCTCCGG GCATGGCTTCCTTGTATGATGGTTCCATGCTGGCTGCCTTGGAGAACGTGGTGGTGGTCA 1665 GCCATGAAGGCTCTAACCTGCCGGTGATGGTGTGGATCCACGGTGGTGCGCTTGTTTTTG CGAACCCGCAGCCTGCATCGCCCTGGGATAACTTGCGAGAAGCCACCTCCTACCCTAATT 390 GGGTCCAAACCTTCCTGGGAATTCCATTTGCCAAGCCACCTCTAGGTCCGCTGCGATTTG crejeaacererreceaerececrifectecrecececreearecerrecearria 330 TGAGGACAAAACCCTCCAAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACTC 1047 AGGTGGTTGCACATTTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCTGCTGAGGTGCC GTGGCGTGGCCCTCCTGCCCGGCCTCATTGCCAGCTCAGCTGA----TGTCATCTCCA GTGGGGTGGCCATCATCCCTTACCTGGAGGCCCATGATTATGAGAAGAGTGAGGACCTGC TGTCTTCGCTTGTTGTGTCCCCCATATCCCAAGGACTCTTCCACGGAGCCATCATGGAGA тсттсеетееевассссаетстетелскатстттееселетссесееваессаталете TCATCCAGTACCGCCTGGGTGTCCTGGGCTTCTTCAGCACTGGAGACAAGCACGCCAACCG 1725 gcrcagccrccarcrrrgargggrccgcccrggcrgccrargaggacgrgriggregie CCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTCCCAGGAGGTGCCTTCAAGACTG TCCCTTCCGACTCCATGTCTGAGGACTGCCTGTACCTCAGCATCTACACGCCGGCCCATA 1545 ACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCACG 507 TGTGTCTACAGGACCTCACCGCAGTGGAGTCAGAGTTTCTTAGCCAGTTCAACATGACCT TGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGA---TCAACACATGCTCAAGGTGCATT CACCCCCTGAGCCCCTGAATCTTGGAGTGGTGAGGGATGGAACCACCCATCCGGCCA 1425 Conservative 16.0%; 0 Score 345.8; DB 3; Pred. No. 2.9e-82; D; Mismatches 617; Indels Length 84; Gaps 2019 987 927 1905 867 1845 627 1605 447 1365 270 807 687 567 1485 ū

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        Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
                                                                                                                                       Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Osanger, A., Fobo, G., Han, M. and Wiemann, S. The German cDNA Consortium
                                                                                                      Direct Submission Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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clone (DKFZp686H0466) is available at the RZPD Deutsches
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Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.

Please contact RZDD for ordering:

http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686H0466
Further information about the clone and the sequencing project is

available at http://mips.gsf.de/projects/cdna/.

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Query Match 15.9%; Best Local Similarity 54.7%; 1354 GGGTCCAAACCTTCCTGGGAATTCCATTTGCCAAGCCACCTCTAGGTCCGCTGCGATTTG 211 GGAACACCAGGCTGGGATGGATTCAGGGCAAGCAAGTCACTGTGCTGGGAAGCCCTGTGC 270 271 crereaacererrecteeacrecerrrectectectecteeartecteearrea 330 TCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACCACATGGGGATCAGCATGCTCCGG GCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCCTATGAGGACGTGCTGGTTGTGG GCCATGAAGGCTCTAACCTGCCGGTGATGGTGTGGATCCACGGTGGTGCGCTTGTTTTTG CCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTCCCAGGAGGTGCCTTCAAGACTG TCCCTTCCGACTCCATGTCTGAGGACTGCCTGTACCTCAGCATCTACACGCCGGCCCATA 1593 CACCCCCTGAGCCCCTGAATCTTGGAGTGTGAGGGATGGAACCACCCATCCGGCCA 1473 GGACCACACACGGGGCAGGTGCTGGGGAGTCTTGTCCATGTGAAGGGCGCCCAATGCCG GCATGGCTTCCTTGTATGATGGTTCCATGCTGGCTGCCTTGGAGAACGTGGTGGTGGTCA 1713 ACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCACG TGTGTCTACAGGACCTCACCGCAGTGGAGTCAGAGTTTCTTAGCCAGTTCAACATGACCT TGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGA---TCAACACATGCTCAAGGTGCATT CGAACCCGCAGCCTGCATCGCCCTGGGATAACTTGCGAGAAGCCACCTCCTACCCTAATT 390 Conservative 0, Score 344.2; DB 3; Pred. No. 8.8e-82; Mismatches 618; Indels 84; Length 3909; Gaps 1653 1533 1413 1353 687 627 567 507 447

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Shultz,M.A., Zhang,L., Gu,Y.-Z., Baker,G.L., Fannuchi,M.V.,
Padua,A.M., Gurske,W.A., Morin,D., Penn,S.G., Jovanovich,S.B.,
Plopper,C.G. and Buckpitt,A.R.

Gene expression analysis in response to lung toxicants: I.
Sequencing and microarray development
Am. J. Respir. Cell Mol. Biol. 30 (3), 296-310 (2004)

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Tel: 530 752 0793

Fax: 530 752 4698
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Average Phred score is 20 or better. All poor quality data (Phred
20) and vector/linker sequence has been removed.
High quality sequence stop: 1918.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CF111083 1918 bp mRNA linear EST 23-JUL-2003 Shultzomica04334 Rat lung airway and parenchyma cDNA libraries Rattus norvegicus cDNA clone Contig3845 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 15.7%; Score 338; DB 7; Length 1918;
Similarity 54.2%; Pred. No. 3.4e-80;
69; Conservative 0; Mismatches 660; Indels 7
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TACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTG 539
                                                 TCAGAGCTTTTCACCAACAGGAAGGAAAACATTCCTTTACAGTTTTCTGAAGACTGCCTC
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/dev stage="adult"
/dev stage="adult"
/clone_lib="Rat lung airway and parenchyma cDNA libraries"
/note="Organ: lung; Vector: pGEM-11Zf(-); Site_1: Eco RI;
Site_2: Not I; mRNA was isolated from microdissected rat
lung airways and parenchyma tissues."
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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GAGC 1568 	1509 TTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACCGGAGGAGGAGGAAGTTACTGAGC
TGCC 1508	1449 AAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTTCGGTGGTG
CACG 1448 	1389 GCTGGTGCACCTGTCTACTCTATGAGTTTCGGCACCGGCCTCAGTGCTTTGAAGACACG
AGAT 1388 AGAT 1342	1329 TTGCTTGGAGATGTGTTCTTTGTGGTCCCTGCACTGATCACAGCTCGATATCACAGAGAT
GGAC 1328 GGAC 1282	1269 GCTAATGAATACTTCCATGACAAGCACTCCCTGACTGAAATCCGAGACAGTCTTCTGGACAGACA
TGTG 1268 1222	1211 TGCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAGTATTTGCACCTTGTG
CCCT 1210	1161 CTGCCTATGAAGGAGGCTCCTGAGATCCTCAGTGGCTCCAACAAGTCCCT
CCTG 1160 GATC 1102	1101 AAAGCATTTAAAGCAATTCCTTCCATCATCGGAGTCAATAACCACGAGTGTGGGCTTCCTG
TCAG 1100 TGAG 1042	1041 TTCACTCGAGTGGTTGATGGTGCTTTTCTTATTGACCTCTAGATCTATTGTCTCAG
CTTC 982	996AAACCCTCCAAGGAGCTGCTGAGCCCTCAGGCAGAAACAAAGTCT 996AAACCCTCCAAGGAGCTGCTGCTGAGCCCTAGCAGAAACAAAGTCT
TTCA 922	960 TCAGACTCTGAGGCCCTGAGGTGCCTGAGGACA
ATGCG 959 CACA 862	900 CATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAATGCG
AGGCC 899 TACA 802	840 GGCTTATTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGAGGCC
CCAAA 839 CCAAG 742	780 TTTGGCGAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCCATGGC
CCATC 779 CCATC 682	720 CTGTCCTGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATC
CTGCT 719 CTGCA 622	660 TTCACCACATGGGATCAGCATGCTCCGGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCT
GTTTC 659 GATTC 562	600 GCTGCCTATGAGGACGTGCTGGTTGTGGTCCTCCAGTACCGGCTAGGAATATTTGGTTTC
CCCTG 599 CCCTC 502	540 TGGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTG
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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotatic of 60,770 full-length cDNAs

L Nature 420, 563-573 (2002)

B 6 (bases 1 to 98)

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Furuno, M., Hizawa, K., Carninci, P., Fukuda, S., Fukunishi, Y., Pruruno, M., Hanagaki, T., Hara, A., Hayateu, N., Hiranoto, K., Hiranoto, K., Tori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,
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20499374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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estis cDNA, RIKEN full-length enriched
product:serine/threonine kinase 33, full
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 17-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
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                                                                                             GCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGAGAAGTTACTG
                                                                                                                                                                                           GATTCTGGTGGACCTGTCTATTTTTATGAGTTTCAGCACAGACCCCATTGCTTTCAAAAC
AGCAGGAAGATGAAATACTGGGCTAACTTTGCCAGGAGCGGGGATCCTAACGGTGCC
                            AGCCGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACCGGGAATCCTAATGGGAAC
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/db_xref="GI:12840657"
/db_xref="GI:12840657"
/translation="MSSMYLFISITCLYVFSSFSVRTSTCLIVFSCFSLRTCNSLAVF
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SCISLSDLLKSFLMSSTIIMRYAFKSRSRFSGYLVCPGLGEVGYLGSDDDSGGFVYFY
BFQHRPHCFQNSRPAFYKADHTDEIRFVFGGFPLKGDVVMFEEATEEEKLLSRKMXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="unnamed protein product; putative
serine/threonine kinase 33 (MGD|MGI:2152419,
evidence: BLASTN, 98%, match=367)"
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SKALLSPTFSLILLSLLSPVLLSAAS"
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'clone_lib="RIKEN full-length enriched mouse
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strain="C57BL/6J"
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db_xref="taxon:10090"
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Pred. No. 3.9e-79;
0; Mismatches 157;
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2038 bp
Mus musculus, clone IMAGE:5123923,
BC019926
                                                                         through the I.M.A.G.E. Consortium/LLNL at: http://i
Series: IRAK Plate: 42 Row: p Column: 20
This clone was selected for full length sequencing
passed the following selection criteria: Similarity
identity to protein
                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I_M.A.G.B. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart
Richards, S., Gibbs, R.A.
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clone has the following problem:
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                      1022 CAGCCAGAAAACAAAGTCTTŢCACTCGAGTGGTTGATGGTGCTTŢCŢŢŢCŢAATGAGCC 1081
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CAAGCAGAAAAACGTGAACATTTCCTACATAGTCAATGACTCCTTCTTCCCACAAAGGCC
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/db_xref="raxon:10090"
/clone="IMAGE:5123923"
/tissue_type="Liver, normal. 5 mc/clone_lib="NCI_CGAP_Li9"
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/note="Vector: pCMV-SPORT6"
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Search completed: June 15, 2005, 02:39:37 Job time: 7174.54 secs

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Sequence 1, Appli
Sequence 155, App
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RESULT 1 US-10-023-515-1 US-10-023-515-1; Sequence 1, Application US/10023515; Patent No. 6664091; GENERAL INFORMATION: APPLICANT: Curtis, Rory A. J. APPLICANT: Silos-Santiago, Inmacu; APPLICANT: S108-Santiago, A NOVEL; TITLE OF INVENTION: 53010, A NOVEL		101.2	101.2	101.2	101.2	101.2	101.2	101.2	101.2	101.2	105.6	105.6	121.4	123	123	123	123	128.6	139.4
plicat 1091 ATION: rtis, ilos-s		4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.9	4.9	5.6	5.7	5.7	5.7	5.7	6.0	6.5
1 Application US/10 664091 RMATION: Curtis, Rory A. C Silos-Santiago, VENTION: 53010, I		2428	2428	2375	2184	2184	1908	1908	1907	1905	836	836	4233	4436	2862	2802	1764	12827	35060
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TITLE OF INVENTION: FAMILY MEMBER AND USES
FILE REFERENCE: 10448-122001
CURRENT APPLICATION UMBER: US/10/023,515
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/256,369
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/279,508
PRIOR FILING DATE: 2000-12-28
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2010-03-28
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RESULT 2
US-10-023-515-3
; Sequence 3, Application US/10023515
; Patent No. 6664091
; Patent No. 6664091
; GENERAL INFORMATION:
APPLICANT: Curtis, Rory A. J.
APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-122001
; CURRENT APPLICATION NUMBER: US/10/023,515
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/256,369
; PRIOR APPLICATION NUMBER: 60/256,369
; PRIOR APPLICATION NUMBER: 60/279,508
; NUMBER OF SEQ ID NOS: 6
; SOFTMARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1746

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; TYPE: DNA
; ORGANISM: Homo
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Best Local Similarity 100.0%;
Matches 1746; Conservative (
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  GATGGTGCTTTCCTTAATGAGCCTCTAGATCTATTGTCTCAGAAAGCATTTAAAGCA 1115
                 AAACCCTCCAAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACTCGAGTGGTT
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                                                  GCACATTTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCTGCTGAGGTGCCTGAGGACA
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                                                                                                  Sequence 155, Application US/09799451 Patent No. 6783969 GENERAL INFORMATION:
 APPLICANT:
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Tang, Y. Tom
Tang, Y. Tom
Zhou, Ping
Goodrich, Ryle
Asundi, Vinod
Ren, Feiyan
Zhang, Jie
Xue, Aidong J.
Zhao, Qing A.
Wang, Jian-Rui
Ma, Yunging
Yamazaki, Victoria
Chen, Rui-hong
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CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt FL_genes Version 2.0
SEQ ID NO 155
LENGTH: 965
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (128)..(925)
US-09-799-451-155
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Best Local Similarity
Matches 675; Conserv
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APPLICANT:
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APPLICANT: Yang, Yonghong
APPLICANT: Wahrman, Tom
APPLICANT: Ghosh, Reena
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6783969el Nucleic
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
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ilarity 81.0%;
Conservative
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Pred. No. 1.8e-141;
0; Mismatches 4;
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NESULT 4

US-09-949-016-3799

Sequence 3799, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTION: BOLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PRILING DATE: 2000-10-3

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ FOR Windows Version 4.0

CORGANISM: Human

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                                                                                                                           ACTIGECCECTETTCGACCAGGAGGAGCAATACCTGCAGCTGAACCTACAGCCTGCGGTGG
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Patent No. 6812339
GENERAL INFORMATION:
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Best Local Similarity
Matches 876; Conserv
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                                                                                                            ACTITIGGAGGCAACCCTGACCGTGTCACCATTTTTTGGCGAGTCTGCGGGTGGCACGAGTG
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RESULT 6
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; Sequence 27, Application
; Patent No. 6800483
; GENERAL INFORMATION:
                               APPLICANT: Danks, Mary K.
APPLICANT: Danks, Mary K.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Metl
TITLE OF INVENTION: Tumor Cells
FILE REFERENCE: SJ-0005
CURRENT APPLICATION NUMBER: US/09/595,68:
CURRENT FILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: 60/075,258
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; PRIOR APPLICATION NUMBER: PCT/US99/03171
; PRIOR FILLING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: Danks, Mary K.
APPLICANT: Potter, Philip M.
APPLICANT: Houghton, Peter J.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: Tumor Cells
FILE REFERENCE: 5J-0005
CURRENT APPLICATION NUMBER: US/09/595,682B
CURRENT FILING DATE: 2000-01-16
FRIOR APPLICATION NUMBER: 60/075,258
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR PILLING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                           Sequence 20, Application US/09595682B Patent No. 6800483 GENERAL INFORMATION:
Query Match
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ORGANISM: Oryctolagus
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Sequence 3, Application US/09264737A

Patent No. 6107549

GENERAL INFORMATION:

APPLICANT: Peng, Paul C.C.

APPLICANT: Ruff, Thomas G.

ITILE OF INVENTION: Engineering Plant Resistance to Pyri

ITILE OF INVENTION: Expression of Esterase Enzymes

PILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance

CURRENT APPLICATION NUMBER: US/09/264,737A

CURRENT PILING DATE: 1999-03-09

EARLIER APPLICATION NUMBER: 60/077,377

EARLIER APPLICATION NUMBER: 50/077,377

EARLIER FILING DATE: 1998-03-10

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3

LENGTH: 1701

TYPE: DNA

ORGANISM: Rabbit

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                                    TGGCCGTCTTCCTGGGAGTCCCCTTCGCCAAGCCCCCTCTTGGATCCCTGAGGTTTGCAC
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Pred. No. 7.5e-96;
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Best Local :
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (1)...(168971)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Human
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Local Similarity 100.0%; Pred. No. 3.7e-40;
hes 176; Conservative 0; Mismatches 0; Indels 0;
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                                                                                            ACAAGGAAGGTTACCTGCAGATTGGAGCCACCCAGGCAGCCCAGAAACTGAAAGACA 1624
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FILE REFERENCE: BTI-45
CURRENT APPLICATION NUMBER: US/09/810,8618
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/190,440
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 5
SOPTWARE: Patentin Ver. 3.1
SEQ ID NO 3
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Best Local
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APPLICANT: Soreq, Hermona
APPLICANT: Arntren, Charles J.
APPLICANT: Mason, Hugh S.
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ACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCC 725
                                   GAGAGGACTGTGCTGGTGCCATGAACTACCGGGTGGGAGCCTTTGGCTTCCTGGCCCTG
                                                                                                              GGCTTCTACAGTGGGGCCTCCTCCTTGGACGTGTACGATGGCCGCTTCTTGGTACAGGCC 1353
                                                                                                                                          GCCTTCAAGACTGGCTCAGCCTC-----CATCTTTGATGGGTCCGCCCTTGGCTGCCTAT 608
                                                                                                                                                                                                                     GCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGGTGGTTCCCAGGAGGT 554
                                                                                                                                                                                                                                                                ACCGAGATGTGGAACCCCAACCGTGAGCTGAGCGAGGACTGCCTGTACCTCAACGTGTGG 1236
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                                                                                                                                                                                     ACACCATACCCCCGGCCTACATCCCCCA----CCCCTGTCCTCGTCTGGATCTATGGGGGT 1293
                                                                                                                                                                                                                                                                                                  CTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTGAACATCTAT 494
                                                                                                                                                                                                                                                                                                                                         ACAACCTTCCAGAGTGTCTGCTACCAATATGTGGACACCCTATACCCAGGTTTTGAGGGC 1176
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ilarity 51.8%;
Conservative
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Pred. No. 2.6e-30;
0; Mismatches 374;
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1056 314 254 942 882

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APPLICANT: ATRIZEN, Charles J.
APPLICANT: MASON, Hugh S.
ITILE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN
ITILE OF INVENTION: TRANSGENIC PLANTS
CURRENT SEPLICATION NUMBER: US/09/810,861B
CURRENT APPLICATION NUMBER: 60/190,440
PRIOR APPLICATION NUMBER: 60/190,440
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/190,440
SEQ ID NO SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 4
LENGTH: 14446
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US-09-810-861B-4
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (11862)..(12157)
OTHER INFORMATION: Description of Artificial Sequence: plasmid vector
OTHER INFORMATION: pTM036. Identity of sequence residues 11862-12157 u
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                   ACAACCTTCCAGAGTGTCTGCTACCAATATGTGGACACCCTATACCCAGGTTTTGAGGGC 480
                                                                                                                       GGACCCCGTCGCTTTCTGCCACCGGAGCCCAAGCAGCCTTGGTCAGGGGTGGTAGACGCT
                                                                                                                                                              GGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTGCGAGAAGCC 374
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                                                                      ACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGATCAACACATG
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Arntzen, Charles J.
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Pred. No. 5.1e-30;
0; Mismatches 374; Indels 18;
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APPLICANT: Mor, Charles J.
APPLICANT: Mor, Charles J.
APPLICANT: Mason, Hugh S.
ITILE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN TILE OF INVENTION: TRANSGENIC PLANTS
ITILE OF INVENTION UNMBER: US/09/810,861B
CURRENT APPLICATION NUMBER: US/09/810,861B
CURRENT APPLICATION NUMBER: 60/190,440
PRIOR APPLICATION NUMBER: 60/190,440
PRIOR FILING DATE: 2000-03-17
INUMBER OF SEG ID NOS: 5
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 5
LENGTH: 1725
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US-09-810-861B-5
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                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: human acetylcholinesterase gene optimized for OTHER INFORMATION: expression in plants
                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                             Local Similarity
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55.1%;
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                                                                                                                                                                                                         Score 139.4; DB 4;
Pred. No. 1.2e-30;
0; Mismatches 266;
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                                                                                                                                                                                                                                                             Length 1725;
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RESULT 13
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                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPAILD16
COMPUTER: IBM PC COMPAILD16
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/732,962A
FILING DATE: 19910722
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 39304/JPW/LSTELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORWATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1845 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Fischer, Meir
TITLE OF INVENTION: EXPRESSION OF ENZYMATICALLY ACTIVE
TITLE OF INVENTION: RECOMBINANT HUMAN ACETYLCHOLINESTERASE
                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White, Esq.
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                 ZIP: 10112
                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                              CITY: New York
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                                                                                                      39304/JPW/LSW
                                                                                                                                                                                                                           Version
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                                                                                                RESULT 14
PCT-US92-06106-1
Sequence 1, Application PC/TUS9206106
Sequence 1 INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fischer, Meir
INTLE OF INVENTION: ENZYMATICALLY A
ITTLE OF INVENTION: ACETYLCHOLINEST
NUMBER OF SEQUENCES: 2
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US-07-732-962A-1
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (ge
FEATURE:
NAME/KEY: CDS
                                                                                     CORRESPONDENCE ADDRESS
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
                                                         STREET:
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                                            ATGGAGAGTGGGGTGGCCA 879
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Pred. No. 1.3e-30;
0; Mismatches 266
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TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1845 base pairs
TYPE: NUCLEIC ACID
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Best Local (
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ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 3930
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06106
FILING DATE: 19920722
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TOPOLOGY: linear
TOPOLOGY: DNA (genomic)
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Similarity 55.1%;
41; Conservative
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| Sequence 1192, Application US/09949016 |
| Patent No. 6812339 |
| GENERAL INFORMATION: |
| APPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| FILE REFERENCE: CLO01307 |
| CURRENT APPLICATION NUMBER: US/09/949,016 |
| CURRENT FILING DATE: 2000-04-14 |
| PRIOR APPLICATION NUMBER: 60/241,755 |
| PRIOR FILING DATE: 2000-10-02 |
| PRIOR APPLICATION NUMBER: 60/237,768 |
| PRIOR APPLICATION NUMBER: 60/231,498 |
| PRIOR APPLICATION NUMBER: 60/231,498 |
| PRIOR PILING DATE: 2000-09-08 |
| NUMBER OF SEQ ID NOS: 207012 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 1192 |
| LENGTH: 2158 |
| TYPE: DNA |
| ORGANISN: Human |
| US-09-949-016-1192 |
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Local Similarity 55.1%;
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                             ATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTATTCCACAAAGCCATC
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                                                                  ATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGCGAGTCCGCGGGAGCC
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Pred. No. 1.5e-30;
0; Mismatches 266;
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Carboxylesterase; enzyme; human; analgesic; nootropic; antiinflammatory; diagnosis; therapy. 27-JUN-2002. Region Protein Homo sapiens. Human carboxylesterase family member 53010. 23-SEP-2002 ABB79537 standard; protein; 18-DEC-2001; 2001WO-US049075. Active-site Domain ABB79537; WO200250256-A2. Peptide (first entry) /note= "p 219. .234 Location/Qualifiers note= label = Mature_protein label= Signal_peptide .545 . 135 "predicted carboxylesterase type-B signature" "carboxylesterase "predicted carboxylesterase type-B serine active 581 8 domain"

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26-SEP-2003
The present invention describes the use of polypeptides related to urological disorders for identifying a compound capable of treating a urological disorder, identifying a subject having a urological disorder, or treating a subject having a urological disorder. Also described: (1) method for identifying a compound capable of treating a urological disorder; (2) a method for identifying a subject having a urological
                                                                        Use of polypeptides related to urological disorders, e.g. 44330, 54211 or for identifying a compound capable of treating a urological disorder or identifying and treating a subject having a urological disorder.
                                                                                                                                                                                                                                                                                                                         urological disorder; uropathic; cytostatic; urinary incontinence; benign prostatic hyperplasia; human.
                                                          Claim
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KW nootropic; neuroprotective; immunosuppressive; haemostatic;
KW antiinflammatory; cardiant; antiincer; virucide; antithyroid;
KW derebroprotective; anorectic; metabolic; vaccine; cancer; infection;
KW wound healing disorders; atherosclerosis; parkinson's disease;
KW Alzheimer's disease; autoimmune disorder; haematopoietic disorder;
KW Alzheimer's disease; autoimmune disorder; haematopoietic disorder;
KW inflammation; neoplastic disease; nervous system disorder;
KW cardiovascular disorders; pancreatitis; respiratory disorder;
KW hyperproliferation; systemic autoimmune disease; hyper-immunity;
KW hyperproliferation; systemic autoimmune disease; hyper-immunity;
KW hyperproliferation; systemic autoimmune disease; hyper-immunity;
KW hematological disease; metabolic disease; sperm dysfunction;
KW hyporoid disease; metabolic disease; sperm dysfunction;
KW thyroid disorder; hypothyroidism; brain damage; colitis;
KW thyroid disorder; pupothyroidism; brain damage; colitis;
KW thyroid disorder; hypothyroidism; brain damage; colitis;
KW thyroid providition disorder; spinal cord; thyroid gland; heart;
KW angiogenesia; ovulation disorder; spinal cord; thyroid gland; heart;
KW trachea; thymus; lymph node; muscular system; obesity; anorexia;
KW growth abnormality; precoccious puberty.
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20-DEC-2000; 2000US-0257048P.
09-JAN-2001; 2001US-0264922P.
30-JAN-2001; 2001US-0264922P.
06-FEB-2001; 2001US-0266797P.
19-MAR-2001; 2001US-0276988P.
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GLAXO GROUP LTD.
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Martensen Agarwal 2002-508784/54. DB; ABQ86169. ָס, SA, Birkeland M, A, Rizvi SK, Cogswell JP, Kabnick KF, Smith RF, Strum JC, Xie Ö

Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorde disorder

Claim 1(a); Page 312-313; 335pp; English.

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The invention relates to an isolated polypeptide with signal sequences contivity of polypeptides of the invention may be described as, cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic, cardiant, antipleer, virucide, antithyroid, cerebroprotective, immunosuppressive, haemostatic, antipalamatory, can detabolic. Polypeptides and polymucleotides of the invention are cuseful in the treatment, or as a vaccine in the prevention of, cancer, commund healing disorders, infection, atherosclerosis, Parkinson's disease and allehemetion, heapplastic disease, autoimmune disorder, heamatopoletic disorder, and allehemetion, neoplastic diseases, nervous system related disorders and cardiovascular disorders, pancreatitis, respiratory disorder, cardiovascular disorders, pancreatitis, respiratory disorder, propositieration, systemic autoimmune disease, hyper-immunity, confidence and diseases, metabolic diseases, sperm dysfunction, thyroid disorders e.g. hypothyroidism, brain damages, colitis, cone photocondition, deficiency, neurological diseases, stroke, angiogenesis,

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Human; drug metabolising enzyme; autoimmune; inflammatory disorder; acquired immunedeficiency syndrome; AIDS; atherosclerosis; psoriasi
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 psoriasis;
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565 1808 545 1748 525 1688 1628 485 1568 465 1508

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proliferative disorder; arteriosclerosis; cirrhosis; hepatitis; cancer; asthma; neurological disorder; Alzheimer's disease; Huntington's disease; dementia; Parkinson's disease; developmental disorder; anaemia; adenoma; drug screening; endocrine disorder; conjunctivitis; glaucoma; cataract; renal tubular acidosis; eye disorder; epilepsy; thrombosis; peptic ulcer; anorexia; metabolic disorder; cystic fibrosis; diabetes; liver disorder; goitre; gastrointestinal disorder; gene therapy; virucide; anticoagulant; anticonvulsant; nootropic; enzyme; DME-10.
Key
Peptide
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13-JUN-2002.

04-DEC-2001; 2001WO-US047429

08-DEC-2000; 2000US-0254308P. 15-DEC-2000); 2000US-0256189P. 21-DEC-2000; 2000US-025713P. 19-JAN-2001; 2001US-0252706P. 02-FEB-2001; 2001US-0266020P.

(INCY-) INCYTE GENOMICS INC.

Sanjanwala MM, Yao Lee EA, Ding L, Ha Lal PG, Warren BA, Yao MG, Au-Young J, Baughn MR, Arvizu C, , Hafalia AJA, Tang YT, Yue H, Tribouley BA, Yang J, Walia NK, Nguyen DB, Gandhi Ring HZ; CM, Lu D; AR, Lu Y; Lu DAM; Lu Y;

WPI; 2002-519668/55. N-PSDB; AAD40574.

Novel human drug metabolizing polypeptide, useful in diagnosis, prevention or treatment of autoimmune/inflammatory, cell proliferative, neurological, developmental, endocrine, metabolic and gastrointestinal

Claim 65; Page 155-156; 169pp; English

The invention relates to an isolated human drug metabolising enzyme (DME) and its nucleotide. DME is useful for diagnosing, treating or preventing conditions of the nucleotide with abstrant expression of DME, where the disorders selected from autoimmune/inflammatory disorder such as acquired immunodeficiency syndrome (AIDS), asthma, atherosclerosis, psoriasis, proliferative disorder such as arteriosclerosis, proliferative disorder such as arteriosclerosis, proliferative disorder such as arteriosclerosis, and cancer; a neurological disorder such as CC already, hepatitis, and cancer; a neurological disorder such as CC already, hepatitis, and cancer; as renal tubular acidosis, epilepsy, astemata; an endocrine disorder such as renal tubular acidosis, epilepsy, an eye disorder such as conjunctivitis, glaucoma, cataract; metabolic disorder such as conjunctivitis, glaucoma, cataract; metabolic disorder such as anorexia, peptic ulcer, and liver disorders. DME is useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. The invention is useful for creating

8	D Q	D dd	, B &) B &	S B 2	. B &) B 5	}	S B 8	}	}	dg VQ	g	US-10	Alignmei Pred. No Score: Percent Best Loo Query Ma DB:	នួននួននួន
966 TCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAACCCTTCCAAGGAGCTGCTGACCCTCAGC 1025	906 TATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAATGCGTCAGAC 965 	846 TTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGAGGCCCATGAT 905 	o—o	72	n 10 a	32 6	12	92 8	1 10 0	»—c	32 F	12 V	186 GGGCCTTCTGCTGAAGGGCCACAGAGGAACACCAGGCTGGGATGGAT	.0-023-515-1 (1-2158) x AAE25025 (1-642)	gnment Scores: 2.74e-273	knock-in humanised animals or transgenic animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in the chromosomal location due to translocation, inversion, etc. among normal, carrier or affected individuals, and as hybridisation probes for mapping naturally occurring genomic sequences. The present sequence is human DME-10 Sequence 642 AA;

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                                                                                                                                                                                                                                                                                                                                                                                         Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel diagnostic and therapeutic polynucleotides CC selected from one of the 2722 sequences defined in the specification. A CC polynucleotide of the invention may have a use in gene therapy. The human CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be CC used to diagnose a particular condition, disease or disorder associated CC with human molecules, e.g. cell proliferative disorder, endocrine CC disorder, neurological disorders, developmental disorders, or CC infections caused by virus, bacteria, fungi or parasite. The dithp CC molecules may also be used in genetic mapping, in identifying individuals CC from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline CC gene therapy. The present sequence represents a dithp protein of the CC invention. Note: The sequence data for this patent is not represented in CC the printed specification, but was obtained in electronic format directly CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy oin gene mapping.
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KW Human; cytostatic; vulnerary; antiarteriosclerotic; antiparkinsonian; KW nootropic; neuroprotective; immunosuppressive; haemostatic; KW antiinflammatory; cardiant; antiulcer; virucide; antithyroid; KW cerebroprotective, anorectic; metabolic; vaccine; cancer; infection; KW wound healing disorders; atherosclerosis; parkinson's disease; KW whilammation; neoplastic disease; nervous system disorder; KW inflammation; neoplastic disease; nervous system disorder; KW cardiovascular disorders; pancreatitis; respiratory disorder; KW hyperproliferation; systemic autoimmune disease; hyper-immunity; KW developmental abnormality; gastrointestinal ulceration; neuropathy; KW developmental abnormality; systemic disease; sperm dysfunction; KW hypoid disease; metabolic disease; sperm dysfunction; KW thyroid disorder; hypothyroidism; brain damage; colitis; cone photo- transduction deficiency; neurological disease; stroke; KW angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart; KW arschea; thymus; lymph node; muscular system; obesity; anorexia; KW growth abnormality; precoccious puberty.
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06-FEB-2001; 2001US-0266797P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated polypeptide with signal sequences complete which allow it to be secreted extracellularly or membrane associated. The contribution of polypeptides of the invention may be described as, culmerary, antiarteriosclerotic, antiparkinsonian, nootropic, consurprotective, immunosuppressive, haemostatic, antiinflammatory, conditions antiulcer, virucide, antithyroid, cerebroprotective, anorectic, conservation in the treatment, or as a vaccine in the prevention of, cancer, conditions and polynucleotides of the invention are conditionable in the treatment, or as a vaccine in the prevention of, cancer, conditionally disorders, infection, atherosclerosis, Parkinson's disease and allreiant system related disorders and cardiovascular disorders, infection, systemic autoimmune disorder, haematopoietic disorders inflammation, neoplastic diseases, nervous system related disorders and cardiovascular disorders, pancreatitis, respiratory disorder, confidently, gastrointestinal ulceration, neuropathy, confidently, gastrointestinal ulceration, neuropathy, confidently, gastrointestinal ulceration, neuropathy, confidently, gastrointestinal ulceration, thyroid disorders, phyperproliferation, systemic autoimmune disease, hyper-immunity, confidently, systemic autoimmune disease, hyper-immunity, confidently, systemic autoimmune disease, hyper-immunity, confidently, systemic autoinmune disease, hyper-immunity, confidently, hypothyroidism, brain damages, colitis, cone phototrandity, system, parkinon, brain damages, colitis, cone phototrandity, system, parkinon, brain damages, colitis, cone phototrandity, system, parkinon, brain damages, colitis, cone phototrandity, system, parkinon, brain damages, storke, angiogenesis, contachea, thymos, land, heart, contachea, thymus, land, heart, contachea, land, heart, contachea, land, heart, contachea, land, heart
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            CCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTC
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                                                                                                                        The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA5433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
                                                                                                               Sequence
                                                                                                                                                                                       New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                  Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                                                          14-SEP-2001;
24-JAN-2002;
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                              CTATTGTCTCAGAAAGCATTTAAAGCAATTCCTTCCATCATCGGAGTCAATAACGACGAG
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03-APR-2001;
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06-APR-2001;
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; 2001US-0281863P.
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2001US-0283725P.
2001US-0285305P.
2001US-0285305P.
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2001US-02858069P.
2001US-0286292P.
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2001US-0294164P.
2001US-02941848P.
2001US-029952P.
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2001US-0318750P.
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2001US-03324802P.
2001US-0332131P.
2001US-033273P.
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Patturajan M, Liu X, Gusev VY, Li L, Vernet CAM, Zerhusen BD
Gorman L, Shenoy Se, Pena CEA, Smithson G, Burgess CE, Gerla
Padigaru M, Shinkets RA, Gangolli EA, Taupier RJ, Casman SJ,
Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ;
Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA; Ellerman <u>.</u>~ Gerlach BD; £ .

N-PSDB; WPI; 2003-046858/04.)B; ABX72267.

New isolated NOVX polypeptide useful for treating atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease and cancer.

Claim ; Page 303; 666pp; English.

The invention relates to human polypeptides, termed NOVX, and the polypurcleotides encoding them. The polypeptides and polynucleotides are useful for diagnosing disease, and screening for potential therapeutic agents. The sequences are useful for treating metabolic disorders, cardiomyopathy, diabetes, hypertension, congenital heart defects, ortic stenosis, atrial septal defect (ASD), atrioventricular canal defect, ductus arteriosus, pulmonary stenosis, subsortic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease, parkinson's disease, immune disorders, haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease and cancer. Sequences ABUS4542-ABUS4647 represent human NOVX polypeptides invention

Sequence 581

Alignment & Pred. No.: Percent Similarity: Best Local Similarity: Score: Scores: 8.96e-244 2597.50 95.07% 94.31% Length:
Matches:
Conservative:
Mismatches: 581 497 4

Query DB:

Match:

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US-10-023-515-1 (1-2158)

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XX Common drug
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KW drug metak
KW antiinflam
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06-OCT-2000;
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09-NOV-2000;
16-NOV-2000;
22-NOV-2000;
30-NOV-2000;
                                                                                                                                                                                                                            drug metabolising enzyme; DME; cytostatic; immunosuppressive; antiinflammatory; endocrine; ophthalmological; gastrointestinal; hepatotropic; cancer; cell proliferative disorder; autoimmune disorder inflammatory disorder; endocrine disorder; eye disorder; endocrine gastrointestinal disorder; liver disorder; metabolic disorder; enzyme;
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           ; 2000US-0236947P.
2000US-0238864P.
2000US-0242323P.
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Best Local Similarity:
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Elliott VS, Gandhi AR, G
Lal P, Lee EA, Lu DAM,
Ring HZ, Sanjanwala MS,
Walsh RT, Warren BA, Xu
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Griffin JA, Hafalia AJA, Ison CH, KI
Nguyen DB, Arvizu C, Policky JL, Rk
Tang YT, Tribouley CM, Narinder WK;
u Y, Yang J, Yao MG, Yue H;
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The invention discloses a polynucleotide comprising a sequence selected CC from 1970 fully defined nucleotide sequences which encode novel CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide CC or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide of the polynucleotide by contacting the polypeptide or peptide or cCC with the antibody of the encoded protein, and observing the binding CC with the antibody of the encoded protein, and observing the binding CC expressible manner and an antisense polynucleotide. The oligonucleotide in an CC expressible manner for synthesising the polynucleotide, or as a probe for detecting the polynucleotide. The oligonucleotide cCC is useful as a primer for synthesising the polynucleotide, or as a probe for detecting the polynucleotide. The polynucleotide and encoded cCC genes may be included in them, for developing a diagnostic marker or compression are useful as pharmaceutical agents and many disease-related cCC genes may be included in them, for developing a diagnostic marker or compression. The genes are involved in tissue and/or cell constitute, or as targets of gene therapy. The genes are involved in tissue and/or cell transcription-related proteins, signal transduction-related proteins, constitute, or as targets of gene therapy. The genes are involved in tissue and/or cell transcription-related proteins, disease-related proteins and genes considered them can be used as indicators for diseases (e.g. osteoporosis, the activity or expression of the encoded protein to treat diseases. The sequence presented is a protein of the invention. Note: Some of the sequence data for this patent is not represented in the printed consideration of fire and the printed consideration of the sequence information supplied by the
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The present sequence represents a cat cauxin protein (I) or its salt, which is cat kidney disease marker. Also described: (1) a partial peptide (II) of (I); (2) a nucleic acid (III) encoding (I) or (II); (3) a vector (IV) comprising (III) or (II) by culturing (V) comprising (III) or (IV); (5) producing (I) or (II) by culturing (V); (6) a antibody (VI) which couples specifically with (I) or (II); (7) diagnosing cat kidney disease which involves measuring (I) quantitatively, and where reduction of amount of (I) indicates presence of the disease; (8) a cat kidney disease diagnostic agent comprising (I) labelling agent, a reagent which measures the biological activity of urinary (I) or (VI); and (9) a cauxin
                                                                                                                                                                                                                              Novel cauxin protein or its salt, useful and for diagnosing cat kidney disease.
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                                                     GlyAspGluArgLysLysAspLeuGlnValLeuAlaArgIleCysGlyCysHisAlaSer
                                                                         GATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAATGCGTCA
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                                                                            04-MAR-2002; 2002JP-00057908
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Alignment Scores: Pred. No.:
                                                                                  The present sequence represents a cat cauxin protein (I) or its salt, which is cat kidney disease marker. Also described: (1) a partial peptide (II) of (I); (2) a nucleic acid (III) encoding (I) or (III); (3) a vector (IV) comprising (III); (4) a transformed host (V) comprising (III) or (II) by culturing (V); (6) a antibody (VI) (CI) producing (I) or (II) by culturing (V); (6) a antibody (VI) (CI) escase which involves measuring (I) quantitatively, and where reduction (CI) famount of (I) indicates presence of the disease; (8) a cat kidney (CI) escase diagnostic agent comprising (I) labelling agent, a reagent which (CI) escaves the biological activity of urinary (I) or (VI); and (9) a cauxin (CI) disease the biological activity of urinary (I) or (VI); and (9) a cauxin (CI) escaves the biological activity of urinary (I) or (VI); and (9) a cauxin (CI) escaves (I) enables detection of cat kidney disease simply and (CI) escaves (I) enables detection of cat kidney disease, and replaces (CC) producted diagnostic methods such as X-ray imaging, ultrasonic imaging, the provides an early marker for the disease, and replaces (CC) producted diagnostic methods such as X-ray imaging, ultrasonic imaging,
                                                                                                                             blood testing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel cauxin protein or its salt, useful as a cat kidney disease marker, and for diagnosing cat kidney disease.
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N-PSDB; ADF50146.
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US-10-023-515-1 (1-2158) x ADF50147 (1-542)

Percent Similarity:
Best Local Similarity:
Query Match:
DB:

5.58e-184 1985.00 83.27% 71.73% 51.27%

Conservative: Mismatches: Indels: Length: Matches:

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                                               TATGAGGACGTGCTTGTGGTCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACC
                                                                        ProGlyGlyAlaPheLysMetGlySerAlaSerSerPheAspGlySerAlaLeuAlaAla
                                                                                    CCAGGAGGTGCCTTCAAGACTGGCTCAAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCC
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                                                                                                                                           CTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACCGGGAATCCTAATGGG
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|TrpValArgAspAsnIleGluPhePheGlyGlyAspProArgSerValThrIlePheGl
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wound healing disorders; atherosclerosis; Parkinson's disease; Alzheimer's disease; autoimmune disorder; haematopoletic disorder; inflammation; nosplastic disease; nervous system disorder; cardiovascular disorders; pancreatitis; respiratory disorder; hyperproliferation; systemic autoimmune disease; hyper-immunity; developmental abnormality; gastrointestinal ulceration; neuropathy; haematological disease; metabolic disease; sperm dysfunction; thyroid disorder; hypothyroidism; brain damage; colitis; cone photo- transduction deficiency; neurological disease; stroke; angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart; trachea; thymus; lymph node; muscular system; obesity; anorexia; growth abnormality; precocious puberty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cytostatic; vulnerary; antiarteriosclerotic; antiparkinsonian; nootropic; neuroprotective; immunosuppressive; haemostatic; antiinflammatory; cardiant; antiulcer; virucide; antithyroid; cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
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sapiens.

Agarwal P, Martensen ָּט SA, Birkeland BA, Rizvi S Cogswell JP, Kabnick KF, Smith RF, Strum JC, Xie Ö ς.

2002-508784/54. DB; ABQ86171.

Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.

Claim 1(a); Page 315; 335pp; English.

The invention relates to an isolated polypeptide with signal sequences CC which allow it to be secreted extracellularly or membrane associated. The activity of polypeptides of the invention may be described as, CC cycostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic, CC neuroprotective, immunosuppressive, haemostatic, antinflammatory, CC cardiant, antiulcer, virucide, antithyroid, cerebroprotective, anorectic, and metabolic. Polypeptides and polymucleotides of the invention are compared to the invention of, cancer, wound healing disorders, infection, atherosclerosis, Parkinson's disease and Alzheimer's disease, autoimmune disorder, haematopoletic disorder, inflammation, neoplastic diseases, nervous system related disorders and cardiovascular disorders, pancreatitis, respiratory disorders, compared to hyperproliferation, systemic autoimmune disease, hyper-immunity, cancer, compared to the cardiovascular diseases, marroad diseases, sperm dysfunction, thyroid disorders e.g. hypothyroidism, brain damages, colitis, cone photoc transduction deficiency, neurological diseases, stroke, angiogenesis,

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GGAGCCACGGAGGAGAAGTTACTGAGCCGGAAGATGATGAAATACTGGGCTACCTTT 1598
                                                                    AspGluValargPheValPheGlyGlyAlaPheLeuLysGlyAspIleValMetPheGlu
                                                                                GATGAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAA 1538
                                    GlyAlaThrGluGluLysLeuLeuSerArgLysMetMetLysTyrTrpAla
                                                                                                        CGGCACCGGCCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCT
                                                                                                                                           GCACTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTT
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                                                                                                                                                                                                                                                                                                CCTTCCATCATCGGAGTCAATAACCACGAGTGTGGCTTCCTGCTGCCTATGAAGGAGGCT 1178
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                                                                                                                                                                              LeuThrGluIleArgAspSerLeuLeuAspLeuLeuGlyAspValPhePheValValPro
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                                                                                                                                                                                                                                                                                                                                                            CCCTCCAAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACTCGAGTGGTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                       CATTTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAA
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RESULT 14
AAB20911
ID AAB20
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Novel human carboxylesterase-like enzyme polypeptide, regulators of which are useful for preventing and treating organophosphorus intoxication, cancer and osteoporosis.

Disclosure; Fig 8; 92pp; English.

The invention relates to a purified human carboxylesterase-like enzyme CC polypeptide. Carboxylesterase-like enzyme and its DNA are useful for CC screening for agents which decrease or modulate the activity of carboxylesterase-like enzyme polypeptide. Carboxylesterase-like enzyme is CC carboxylesterase-like enzyme polypeptide. Carboxylesterase-like enzyme is CC disease, such as organophosphorus intoxication, cancer and osteoporosis. CC compounds that increase the ability of human carboxylesterase-like enzyme cc to bind to organophosphorus compounds are useful as detoxifying agents. CC carboxylesterase-like enzyme agonists and antagonists are useful for CC particularly dental implants. Carboxylesterase-like enzyme is useful in CC diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases or abnormalities related to the presence of cutations in the nucleic acid sequences which encode the enzyme. The CC in gene therapy and for generating antisense oligonucleotides or carboxylesterase-like enzyme polynucleotides or carboxylesterase-like enzyme polynucleotides or carboxylesterase-like enzyme polynucleotides or carboxylesterase-like enzyme polynucleotides are useful for modulating carboxylesterase-like enzyme gene expression. The CC useful for modulating carboxylesterase-like enzyme gene expression. The present sequence is rat carboxylesterase-like enzyme protein

Sequence 561 AA;

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                                                                                                                        ThrSerValSerSerHisValIleSerProMetSerGlnGlyLeuPheHisGlyAlaIle
                                                                                                                                   ATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTATTCCACAAAGCCATC
                                                                                                                                                              ATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGCGAGTCCGCGGGAGCC
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ThrThrHisThrGlyGlnValGlnGlyLysLeuAspHisValLysAspThrLysAlaGly
            CTGAGGTGCCTGAGGACAAAACCCTCCAAGGAGCTGCTGAGCCCTCAGCCAGAAAAACAAAG
                                                            GACCTGCAG----GTGGTTGCACATTTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCTG
                                                                              ATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGAGGCCCATGATTATGAGAAGAGTGAG
                                                                                                                                                                                                     CysLeuGlnAsnLeuAspIleLeuAspGluValGlyLeuLeuAspMetLysMetIle---
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                                        ThrValSerThrThrValAlaLysLeuSerGlyCysGluAlaMetAspSerGluAlaLeu
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                  Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetc; antiinflammatory; antiulcer; vulnerary; anticonvulsant antibacterial; antifungal; antiparasitic; cardiant; immune disorder; addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease.
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sapiens

ovarian

cancer associated antigen protein sequence SEQ

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anticonvulsant;

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                                                                                                                                                                                                                                                                                                                                                                                                        Sequences AAF21614 - AAF22031 represent DNA sequences encoding human CC proteins AAB59121 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the CC isolation and characterisation of the DNA and protein sequences of the CC invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; nontropic; antinflammatory; antiulcer; vulneray; anticonvulsant; antidabetic; antifulgal; antiparastic and cardiant activity. The polynucleotide and CC antifungal; antiparastic and cardiant activity. The polynucleotide and CC protein sequences are used in the diagnosis of cancer, particularly conditions agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's diagnosis, prevantion and treatment CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; infertions dispasses such as cerebral anoxia and epilepsy; and
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                                               ArgAspGlyThrThrHisProAlaMetCysLeuGlnAspLeuThrAlaValGluSerGlu
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CACGCTGATGAAGTCCGCTTTGTGTTCCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATG
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|GluPheGlnHisGlnProSerTrpLeuLysAsnIleArgProProHisMatLysAlaAsp
                                                                           GAGTTTCGGCACCGGCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGAC
                                                                                                      IleProAlaLeuGlnValAlaHisPhe---GlnCysSerArgAlaProValTyrPheTyr
                                                                                                                                GTCCCTGCACTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTAT 1412
                                                                                                                                                            GlyAspProGlnThrLeuGlnAlaGlnPheGlnGluMetMetAlaAspSerMetPheVal
                                                                                                                                                                                    ATCCTGCACATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAG 1292
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                                                                                                                                                                                                                                                                                            GAGGCTCCTGAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAAC 1232
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|ValMetValTrpIleHisGlyGlyAlaLeuValPheGlyMetAlaSerLeuTyrAspGly
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Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlh
-Q=/cgn2 1/USPTO_spool/664091/runat_14062005 133459 9346/app_query.fasta_1.4238
-DB=PIR 79 -QPMT=fastan -SUFFIX=n2p.rpr -MINWATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=Dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MN10 - ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=6664091 @CGN 1 101 @runat 14062005 133459 9346 -NCPU=6 -ICPU=3
-NO_MAAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
-DEV_TIMEOUT=170 -WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOP=6
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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ALIGNMENTS

RESULT 1 A47162 밁 Ś 문 ঠ A;Cross-references: UNIPROT:Q04791; GB:L05493; NID:g213100; PIDN:AAA49223.1; PID:g213101 C;Superfamily: cholinesterase; cholinesterase homology C;Keywords: hydrolase A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-557 <HWA> R;Hwang, C.S.; Kolattukudy, P.E.
J. Biol. Chem. 268, 14278-14284, 1993
A;Title: Molecular cloning and sequencing of thioesterase
A;Title: molecular cloning and sequencing of thioesterase
A;Teference number: A47162; MUID:93300823; PMID:8314791
A;Accession: A47162 thiolesterase B (EC 3.-.-.) precursor - mallard C;Species: Anas platyrhynchos (mallard) C;Date: 05-May-1995 #sequence_revision 05-May-1995 Percent Similarity:
Best Local Similarity:
Query Match: US-10-023-515-1 (1-2158) x A47162 (1-557) Pred. No.: Alignment Scores: F;56-545/Domain: cholinesterase homology <CHE> C;Accession: A47162 243 CAAGTCACTGTGCTGGGAAGCCCTGTGGAACGTGTTTCCTCGGAAGTCCCCTTTTGCT 302 303 GCTCCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAAC 362 43 GinvalLysvalAsnAlaAlaGluArgSerValAsnValPheLeuGlyLeuProPheAla 7.1e-91 1298.50 62.77% 48.36% 33.54% Length: Matches: 05-May-1995 #text_change 09-Jul-2004 Gaps: Mismatches: Indels: Conservative: 557 265 79 177 27 ₩ CDNA and stimulation of expre 62

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GTGTTCTTTGTGGTCCCTGCACTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCT 1400
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                                                                                                                                                                           PheProGluPheThrGluGlyLeuGluLysAspValAlaArgGlnValLeuGlnSerThr 375
                                                    IleGlyValAlaGluAsnArgAlaGlnValArgAspGlyLeuLeuAspSerIleAlaAsp
                                                                      LeuAlaLeuSerPheLysGlyAlaProSerAspIleValAspLeuValTyrAsnGluTyr
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C;Superfamily: cholinesterase; cholinesterase home
C;Keywords: carboxylic ester hydrolase
F;32-517/Domain: cholinesterase homology <CHE>
F;201,430/Active site: Ser, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
A34329
60K esterase (EC 3.1.1.-) isoform 2 - rabbit
C. Species: Oryctolagus cuniculus (domestic rabbit)
C. Date: 22-Jun-1990 #sequence_revision 22-Jun-1990
C. Accession: A34329
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A; Title: Isolation,
A; Reference number:
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                                                     CTGCTGCCT----ATGAAGGAGGCT
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ProAlaMetCysLeuGlnAsn-----LeuAlaIleMetAspGlnAspValLeuLeuLeu
                                                                                       GCACTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carboxylesterase (EC 3.1.1.1) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JC5408
R;Schwer, H.; Langmann, T.; Daig, R.; Becker, A.; Aslanidis, C.; Schmitz, G.
Biochem. Biophys. Res. Commun. 233, 117-120, 1997
A;Title: Molecular cloning and characterization of a novel putative carboxylesterase, A;Reference number: JC5408; MUID:97289502; PMID:9144407
A;Accession: JC5408; MUID:97289502; PMID:9144407
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Pred. No.:
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A;Cross-references: GDB:9959011
C;Superfamily: cholinesterase; cholinesterase homology
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A; Residues: 1-559 <SCH>
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                    CGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAAC-----TCAGAG
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ArgAspGlyThrThrHisProAlaMetCysLeuGlnAspLeuThrAlaValGluSerGlu 105
                                                                    CCCCCGCTGGGATCCCTGCGATTTACGAACCCCGCAGCCTGCATCGCCCTGGGATAACTTG 365
                                                                                                                                              ValHisValLysGlyAlaAsnAlaGlyValGlnThrPheLeuGlyIleProPheAlaLys 65
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Conservative:
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GAGTTTCGGCACCGGCCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGAC
                                                      GTCCCTGCACTGATCACAGCTCGATATCACAGAGATGCTGGTGGACCTGTCTACTTCTAT
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                                                                                                                                                                  LeuLeuMetLeuProProThrPheGlyAspLeuLeuArgGluGluTyrIleGlyAspAsn
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| IleValGlyValAsmAsmAsmGluPheGlyTtpLeuIleProLysValMetArgIleTyr 357
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S47655
Carboxylesterase (EC 3.1.1.1) precursor - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 26-Dec-1994 #sequence_revision 03-Aug-1995 #text_c
C;Accession: S47655
R;Sone, T.; Isobe, M.; Takabatake, E.; Wang, C.Y.
Biochim. Biophys. Acta 1207, 138-142, 1994
A;Title: Cloning and sequence analysis of a hamster liver
A;Reference number: S47655; MUID:94318665; PMID:8043605
A;Accession: S47655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-561 <SON>
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CCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG 365
                                                                                                                                                                                                                         GICACIGIGCIGGAAGCCCIGIGCCIGIGAACGIGITCCICGGAGICCCCTTIGCIGCI 305
                                                    SerLysGluArgLysIleIleLeuProThrIleSerMetSerGluAspCysLeuTyrLeu 125
                                                                                CAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTG
                                                                                                         ArgAspGlyThrSerGluProAlaMetCysLeuGlnThrAspPheMetArgProGlnIle 105
                                                                                                                                 CGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGAT
                                                                                                                                                                                                                                                                                              HisArgLeuGlnPheTrpLysLysAlaLeuPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACGCTGATGAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATG
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Matches:
Conservative:
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GluLeuLeuAlaSerValAspPheHisProValProSerIleIleGlyValAspSerAsp 344
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                                                                                                    ProGlnThrLeuGlnAlaGlnPheArgGluLeuMetLysAspPheMetPheValllePro
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                                                                                                                                                                                                                                                                                                                                                                          GluCysGlyTrpGlyValProLeuPheMetGlyLeuAspHisValIleLysAsnIleThr 364
                                                                                                                                                                                                                                                                                                                                                                                                      GAGTGTGGCTTCCTGCCTATG-------AAGGAGGCT 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlnValPheIleMetThrProGlyValValAspGlyIlePheLeuProArgHisProGln
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                       GTTATGTTCGAAGGAGCCACGGAGGAGGAGGAGGTTACTGAGCCCGGAAGATGATGAAATAC 1586
                                                                                                                              CGGCACCGGCCTCAGTGCTTT-----GAAGACACGAAGCCGGCTTTTGTCAAAGCCGAC
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                                                  HisGlyAspHisValAlaPheValPheGlySerAspPheTrpGlyLeuLysIleAspLeu
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-554 <AID>
A;Cross-references: UNIPROT:Q63880; GB:S64130; NID:g404388; PIDN:AAB27606.1; PID:g404389
A;Cross-references: UNIPROT:Q63880; GB:S64130; NID:g404388; PIDN:AAB27606.1; PID:g404389
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase
F;46-536/Domain: cholinesterase homology <CHE>
F;415,443/Active site: Ser, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
S34607
carboxylesterase (EC 3.1.1.1) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S34607
R;Aida, K.; Moore, R.; Negishi, M.
Biochim. Biophys. Acta 1174, 72-74, 1993
Biochim. Biophys. Acta 1174, 72-74, 1993
A;Title: Cloning and nucleotide sequence of a novel, male-predominant carboxylesterase
A;Heference number: S34607; MUID:93326638; PMID:7916639
A;Accession: S34607; MUID:93326638; PMID:7916639
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DB:
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Best Local Similarity:
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ATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTGAACATC
                                                                                                                                                                                                                                                                                                                                                                                                       TATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGGTGGTTCCCAGGA 551
                                                                                                                                                                                                                                                                                     GCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGATCAACAC
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                         ACCTTTGCTCGAACCGGGAATCCTAATGGGAACGACCTGTCTCTGTGGCCAGCTTATAAT 1652
                                                                                     SerGluAsnAlaphevalpheGlyGlyProPheLeuThrAspGluSerSerLeuLeuAla
                                                                                                                                                                                GATGAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTG-----AAGGGGGACATTGTTATG
                                                                                                                                                                                                           CTGACTGAAATCCGAGACAGTCTTCTGGACTTGCTTGGAGATGTGTTCTTTGTGGTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnGluAspLeuLeuGluAsnSerArgProLeuLeuAlaHis-------Met 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTGAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAACATCCTG 1238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlnGlyAsnIleAlaProPheGlyGlyAspProAsnCysValThrIlePheGlyAsnSer
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Best Local Similarity:
Query Match:
DB:
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A,Molecule type: mRNA
A,Residues: 1-554 <OVN>
A,Cross-references: UNIPROT: P23953; GB:M57960; NID:g192853;
C,Superfamily: cholinesterase; cholinesterase homology
C,Keywords: carboxylic ester hydrolase
C,Keywords: carboxylic ester hydrolase
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A39060
Carboxylesterase (EC 3.1.1.1) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 09-Jul-2004
C;Accession: A39060
R;Ovnic, M.; Tepperman, K.; Medda, S.; Elliott, R.W.; Stephenson, D.A.; Grant, S.G.; (Genomics 9, 344-354, 1991
A;Ritle: Characterization of a murine cDNA encoding a member of the carboxylesterase (A;Reference number: A39060; MUID:91169540; PMID:1840565
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                                                          GlyLeuVallleGlyGlyArgSerProTyrAsnGlyLeuAlaLeuSerAlaHisGluAsn 162
                                                                                                                      GCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGTTCCCAAGAGGT :::||||||
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serProAlaAspLeuThrLysSerSerGInLeuProValMetValTrpIleHisGlyGly
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ThrGluLy8GluIleLeuProLeuLy8IleSerGluAspCy8LeuTyrLeuAsnIleTyr
                                                                            GCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTTAGCGTACGAGGAC
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|GlnLeuGluGlnTyrLeuGluIleGlyLeuGluProArgThrGlyValLyBLeuLyBLy8 524
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

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PIDN:AAA63297.1; PID:g192854

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                                   CAGCTGGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTGGATTTTTGG 1730
                                                                                                                                        GluGluThrAsnLeuSerLysMetValMetLysPheTrpAlaAsnPheAlaArgAsnGly
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   GinIleGlyAlaThrThrGlnGlnAlaGlnArgLeuLysAlaGluGluValAlaPheTrp
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A;ACCESSION: $23607
A;Molecule type: protein
A;Residues: 19-40 <MAT2>
A;Note: 28-Lys and 33-Leu were also found
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glyc
E;1-18/Domain: signal sequence #status predicted <SIG>
F;19-56/Product: carboxylesterase #status experimental <MAT>
F;19-552/Domain: cholinesterase homology <CHE>
F;51-552/Domain: cholinesterase homology <CHE>
Transition site: carbohydrate (Asm) (covalent) #status predicted
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A;Title: The nucleotide and
A;Reference number: S19307;
A;Accession: S19307
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N;Alternate names: proline-beta-naphthylamidase
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
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A; Residues: 1-566 < MATI>
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R;Matsushima, M.; Inoue, H.; Ichinose, M.; Tsukada, S.; Miki, K.; Kurokawa, K.;
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ProValMetValTrpIleHisGlyGlyGlyGlyLeuValLeuGlyGlyAlaProMetTyrAsp
                                   CCCGTCTTGGTGTGGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGAT 587
                                                                                      GAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTC
                                                                                                                                          AspLeuPheThrAsnGlyLysGluArgLeuThrLeuGluPhe-----
                                                                                                                                                                          GAGTGGCTGCTCTTAGATCAACACACGTGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCA 467
                                                                                                                                                                                                                                              GAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAAC-----
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SerValPheGlyPheProLeuLeuLysGlyAsp-------AlaProGlu
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                          GluGluValSerLeuSerLysThrValMetLysPheTrpAlaAsnPheAlaArgSerGly
                                       GAGGAGAAGTTACTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACCGGG
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|GlnGluPheGlyTrpLeuLeuProThrMetMetGlyPheProLeuSerGluGlyLysLeu 372
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                                                                                                                                                                                                                                                                                                      GluLeuThrProValAlaThrAspLysTyrLeuGlyGlyThrAspAspProValLysLys 412
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A; Molecule type: mRNA
A; Residues: 1-549 <TAK>
A; Residues: 1-549 <TAK>
A; Experimental source: liver
C; Superfamily: cholinesterase; cholinesterase homology
C; Keywords: carboxylic ester hydrolase; glycoprotein; microsor
F; 1-18/ Dromain: signal sequence #status predicted <SIG>
F; 19-54/ Product: carboxylesterase E1 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-023-515-1 (1-2158) x JX0054 (1-549)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;50-538/Domain: cholinesterase homology <CHE>
F;79,274,302,375,476/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;221,453/Active site: Ser, His #status predicted
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JX0054

Carboxylesterase (EC 3.1.1.1) El precursor, minor form - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_char
C;Accession: JX0054
R;Takagi, Y:, Morohashi, K.; Kawabata, S.; Go, M.; Omura, T.
J. Biochem. 104, 801-806, 1988
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Best Local Similarity:
Query Match:
DB:
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TGGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCTTTGATGGGTCCGCCCTG
                                                                   TyrLeuAsnileTyrSerProAlaAspLeuThrLysAsnSerArgLeuProValMetVal
                                                                                                     TACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTCGTG
                                                                                                                                                                    ThrGlyLysGluSerIleProLeuGluPhe--
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                                                                                                                                                                                                                                                                                                      TACCCTAATTTGTGCCTCCAGAAC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCTTTGCTGCTCCCCCGCTGGGATCC 320
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                                                                                                                                                                                                                                                                  CACCGGCCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACGCTGAT 148:::||||||
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                                                                                                                                                                                                                                                                                                                          ValLeuMetSerArgSerLeuArgAspAlaGlyAlaProThrTyrMetTyrGluPheGln 435
                                                                                                                                                                                                                                                                                                                                                 CTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTCGG 1421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAATGCG 959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAGACTCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAAACCCTCCAAGGAGCTGCTGACC 1019
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A;Molecule type: mRNA
A;Rosidues: 'G',65-185,'G',187-361,363-567 <ZSC>
A;Residues: 'G',65-185,'G',187-361,363-567 <ZSC>
A;Cross-references: GB:X52973; NID:g36421; PIDN:CAA37147.1; PID:g1335304
A;Gdne 108, P.W.; Richards, L.J.; Bowles, M.R.; Pond, S.M.
Gene 108, 289-292, 1991
A;Title: Cloning and analysis of a cDNA encoding a human liver carboxylesterase.
A;Reference number: PS0280; MUID:92084150; PMID:1748313
A;Accession: PS0280
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A; Molecule type: mRNA
A; Residues: 61-567 < LON>
A; Cross-references: GB:M55509; NID:g179929; PIDN:AAA35650.1; PID:g179930
A; Cross-references: GB:M55509; NID:g179929; PIDN:AAA35650.1; PID:g179930
A; Schibata, F.; Takagi, Y.; Kitajima, M.; Kuroda, T.; Omura, T.
Genomics 17, 76-82, 1993
A; Title: Molecular cloning and characterization of a human carboxylesterase
A; Title: Molecular cloning and characterization of a human carboxylesterase
A; Reference number: A47376; MUID:94010913; PMID:8406473
A; Accession: A47376
A; Accession: A47376
A;Molecule type: mRNA
A;Residues: 1-55, G',57-361,363-535,'G',537-567 <KRO1>
A;Cross-references: GB:L07765; NID:g180949; PIDN:AAA35711.1;
A;Accession: A48809
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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A41010

carboxylesterase (BC 3.1.1.1) precursor, monocyte/macrophage [validated] - human N,Alternate names: carboxylesterase, hepatic; monocyte/macrophage serine esterase C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A41010, JH0327; A47376; A49816; BS0280; I61085; A48809; I57004
C;Munger, J.S.; Shi, G.P.; Mark, E.A.; Chin, D.T.; Gerard, C.; Chapman, H.A.
J. Biol. Chem. 266, 18832-18838, 1991
A;Reference number: A41010; MUID:92011649; PMID:1918003
A;Accession: A41010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: liver
A;Note: differences between this sequence and other reports appear to be due to frameshil
R;Kroetz, D.L.; McBride, O.W.; Gonzalez, F.J.
Biochemistry 32, 11606-11617, 1993
A;Title: Glycosylation-dependent activity of baculovirus-expressed human liver carboxyles
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A;Molecule type: mRNA; DNA
A;Roseidues: 1-3; PALIV', 8-11,'A',13-567 <SHI>
A;Roseidues: 1-3; PALIV', 8-11,'A',13-567 <SHI>
A;Cross-references: GB:D21088; NID:9455476; PIDN:BAA04650.1; PID:9458470
A;Cross-references: GB:D21088; NID:9455476; PIDN:BAA04650.1; DID:9458470
A;Cross-references: GB:D21088; NID:9455476; PIDN:BAA04650.1; DID:9458470
A;Note: sequence extracted from NCBI backbone (NCBIP:137630) and corrected to correst A;Note: sequence extracted from NCBI backbone (NCBIP:137630) and corrected to correst A;Note: sequence extracted from NCBI backbone (NCBIP:137630) and corrected to correst A;Note: sequence extracted from NCBI backbone (NCBIP:137630) and corrected to correst A;Note: sequence extracted from NCBI backbone (NCBIP:137630) and corrected to correst A;Note: sequence extracted from NCBI backbone (NCBIP:137630) and corrected to correst A;Note: sequence extracted from NCBI backbone (NCBIP:137630) and corrected to correst A;Note: sequence extracted from NCBI backbone (NCBIP:137630) and corrected to correst A;Note: sequence extracted from NCBI backbone (NCBIP:137630) and corrected to correst A;Note: sequence extracted from NCBI backbone (NCBIP:137630) and corrected to correct A;Note: sequence extracted from NCBI backbone (NCBIP:137630) and corrected to correct A;Note: sequence extracted from NCBI backbone (NCBIP:137630) and corrected to correct A;Note: sequence extracted from NCBI backbone (NCBIP:137630) and corrected to correct A;Note: sequence extracted from NCBI backbone (NCBIP:137630) and corrected to correct A;Note: sequence extracted from NCBI backbone (NCBIP:137630) and corrected to correct A;Note: sequence extracted from NCBI backbone (NCBIP:137630) and corrected to correct A;Note: sequence extracted from NCBI backbone (NCBIP:137630) and corrected to correct A;Note: sequence extracted from NCBI backbone (NCBIP:137630) and corrected from NCBI backbone (NCBIP:137630) and corrected from NCB
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A;Title: Cloning and sequencing of a human liver carboxylesterase isoenzyme.
A;Reference number: JH0327; MUID:91148424; PMID:1997784
A;Accession: JH0327; MUID:91148424; PMID:1997784
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A;Residues: 114,'H', 116-280,'A',282-300,'IGNSYLWTYRETQREST',318-336,'R',338-382,'GSPI',
A;Cross-references: GB:M65261; NID:g187028; PIDN:AAA83932.1; PID:g187029
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A;Title: cDNA cloning and characterization of human monocyte/macrophage serine esterase-l
A;Reference number: A49816; MUID:91300111; PMID:2070086
A;Accession: A49816
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A; Residues: 1-567 < MUN>
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C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum; li
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-145/Domain: propeptide #status predicted <PRO>
F;50-553/Domain: cholinesterase homology <CHB>
F;146-567/Product: carboxylesterase homology <CHB>
F;146-567/Region: endoplasmic reticulum retention signal #status
F;521,468/Active site: Ser, His #status predicted
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A;Cross-references: GB:L07764; NID:g180947; PIDN:AAA16036.1;
C;Genetics
A;Gene: GDB:CES1; HMSE
A;Cross-references: GDB:128044; OMIM:114835
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GlyGluSerAlaGlyGlyGluSerValSerValLeuValLeuSerProLeuAlaLysAsn
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carboxylesterase (EC 3.1.1.1) ES-4 precursor N;Alternate names: hydrolase B C;Species: Rattus norvegicus (Norway rat) C;Date: 28-Oct-1996 #sequence_revision 13-Mac;Accession: S62788; S51203; A55304; S49257 R;Robbi. M.; van Schaftingen, E.; Beaufay, F Biochem. J. 313, 821-826, 1996
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A;Residues: 19-48 cMOR>
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A;Commental source: liver
R;Yan, B.; Yang, D.; Brady, M.; Parkinson, A.
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A;Title: Rat kidney carboxylesterase. Cloning, sequencing, cellular localization, and re
A;Title: Rat kidney carboxylesterase. Cloning, sequencing, cellular localization, and re
A;Title: Rat kidney carboxylesterase. Cloning, sequencing, cellular localization, and re
A;Title: Rat kidney carboxylesterase. Cloning, sequencing, cellular localization, and re
A;Title: Rat kidney carboxylesterase. Cloning, sequencing, cellular localization, and re
A;Reference number: A55304
A;Accession: A55304
A;Molecule type: mRNA
A;Residues: 1-6;F', 8-59,'P', 61-212,'A',214-252,'T',254-309,'IT',312-341,'N',343-424,'FY
A;Cross-references: GB:U10697; NID:9550819; PMID:7961958
A;Accession: A55304
A;Molecule type: mRNA
A;Residues: 1-6;F', 8-59,'P', 61-212,'A',214-252,'T',254-309,'IT',312-341,'N',343-424,'FY
A;Accession: A5504
A;Molecule type: mRNA
A;Residues: 1-56;P', 8-59,'P', 61-212,'A',214-252,'T',254-309,'IT',312-341,'N',343-424,'FY
A;Accession: A5504
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A;Molecule type: mRNA
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GCCCTCCATCTGATACAA-----AACATCCTGCACATCCCGCCTCAGTATTTGCAC 1262
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ThrAsnArgLysGluLysIleHis-----LeuGluPheSerGluAspCysLeuTyr
                                         AGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTTCGGCACCGGCCTCAGTGCTTTGAA
                                                                                                                                                                                                                                                                              CTGCTGCCT-----ATGAAGGAGGCTCCTGAGATCCTCAGTGGCTCCAACAAGTCCCTT 1211
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                                                                                                                                     LeuAlaPheIleGlyAspValSerPheSerIleProSerValMetValSerArgAspHis
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456

ProGlnArgProLysHisValValGlyAspHisAlaAspAspLeuTyrSerValPheGly

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RESULT 11

A55281

Carboxylesterase (EC 3.1.1.1) egasyn - mouse

N;Alternate names: beta-glucuronidase endoplasmic reticulum-targeting protein; esterase-
C;Species: Mus musculus (house mouse)
C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C;Accession. A55281
R;Ovnic, M.; Swank, R.T.; Fletcher, C.; Zhen, L.; Novak, E.K.; Baumann, H.; Heintz, N.;
A;Ovnic, M.; Swank, R.T.; Fletcher, C.; Zhen, L.; Novak, E.K.; Baumann, H.; Heintz, N.;
A;Ovnic, M.; Swank, B.S., 1991
A;Fitle: Characterization and functional expression of a cDNA encoding egasyn (esterase-
A;Reference number: A55281; MUID:92147141; PMID:1783403
A;Reference number: A55281; MUID:92147141; PMID:1783403
A;Residues: Dreliminary
A;Molecule type: mRNA; protein
A;Residues: 1-562 <OVN>
A;Cross-references: UNIPROT:Q64176; GB:S80191; NID:g244727; PIDN:AAB21335.1; PID:g244728
A;Note: sequence extracted from NCBI backbone (NCBIN:80191, NCBIP:80194)
C;Superfamily: cholinesterase; cholinesterase homology
C;Superfamily: cholinesterase; cholinesterase homology
F;51-552/Domain: cholinesterase homology <CHE>
F;222,467/Active site: Ser, His #status predicted
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Best Local Similarity:
Query Match:
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                  TACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTG
                                                                                                              LysAsnAlaThrSerTyrProProMetCysPheGlnAspProValThrGlyGlnIleVal
                                                                                                                                                                     CCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG
                                                                                  CAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTG-----TCAGAAGACTGCCTC
                                                                                                                                         CGAGAAGCCACCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGAT
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       AlaProIleLeuArgGly----
                            GGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGGAGGAGGAGGAGGAGGAGGAGTTA 1562
                                                                                                                                          AGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTGCTTTGAA 1442
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                                                                                                                  ArgAspAlaGlyAlaProThrTyrMetTyrGluPheGlnTyrSerProSerPheSerSer 456
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carboxylesterase (EC 3.1.1.1) precursor - rat (fragment) C;Species: Rattus norvegicus (Norway rat) C;Cate: 21-May-1990 #sequence_revision 03-Aug-1992 #text_change 09-Jul-2004 C;Accession: A31584 R;Long, R.M.; Satoh, H.; Martin, B.M.; Kimura, S.; Gonzalez, F.J.; Pohl, L.R. Biochem. Biophys. Res. Commun. 156, 866-873, 1988 A;Title: Rat liver carboxylesterase; cDNA cloning, sequencing, and evidence for A;Reference number: A31584; MUID:89050119; PMID:2973315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-540 <LON>
A; Residues: 1-540 <LON>
A; Residues: 1-540 <LON>
A; Cross-references: UNIPROT: P10959; GB:M20629; GB:X13587; NID:g203279; PIDN:A
C; Superfamily: cholinesterase; cholinesterase homology
C; Keywords: carboxylic ester hydrolase; glycoprotein
F; 1-9/Domain: signal sequence #status predicted <SIG>
F; 10-540/Product: carboxylesterase #status predicted <MAT>
F; 41-529/Domain: cholinesterase homology <CHE>
F; 41-529/Domain: cholinesterase homology <CHE>
F; 70, 265, 266, 293, 366, 467/Binding ster: carbohydrate (Asn) (covalent) #status
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   TGGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTG
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                             TyrLeuAsnIleTyrSerProAlaAspLeuThrLysAsnSerArgLeuProValMetVal
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                                                                                                        GluIlePheSerValPheGlyThrProPheLeuLys------GluGly
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R;Yan, B.; Yang, D.; Parkinson, A.
Arch. Biochem. Biophys. 317, 222-234, 1995
A;Title: Cloning and expression of hydrolase C, a member of the rat carboxylesterase fam
A;Reference number: S71597; MUID:95177656; PMID:7872788
A;Recession: S71597
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-561 <YAN>
A;Residues: 1-561 <YAN>
A;Residues: 1-561 <YAN>
A;Reperimental source: liver; endoplasmic reticulum
C;Function:
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; liver
F;1-18/Domain: signal sequence #status predicted <SIGS
F;1-561/Product: carboxylesterase #status predicted <AGN>
F;50-561/Region: endoplasmic reticulum retention signal
F;79,301/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;79,301/Binding site: carbohydrate (Asn) (covalent) #status predicted
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S71597
carboxylesterase (EC 3.1.1.1) precursor, liver - rat
N;Alternate names: hydrolase C
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 13-Sep-1998
C;Accession: S71597
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                                                                        GACTGCCTCTACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCC
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LysAsnThrThrTyrProProMetCysSerGlnAspAlaThrLysGlyGlnArgMet
                                                     AspCysLeuTyrLeuAsnIleTyrThrProAlaAspPheThrLysAspSerArgMetPro
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Indels:
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GAGGAGAAGTTACTGAGCCGGAAGATGATGATGATACTGGGCTACCTTTGCTCGAACCGGG
                                                                                        TTTGTGTTCCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAG
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                                                             ServalPheGlyAlaProIleLeuArg-----
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                                                                                                                                                                                  SerArgAspHisArgAspAlaGlyAlaProThrTyrValTyrGluTyrGlnTyrTyrPro
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A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 503-554,'R',556-561 <MED>
A;Cross-references: EMBL:X65295; NID:g57557; PIDN:CAA46390.1;
C;Superfamily: cholinesterase; cholinesterase homology
C;Superfamily: cholinesterase; cholinesterase; G;Superfamily: cholinesterase; glycoprotein
C;Hoywords: carboxylic seter hydrolase; glycoprotein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-561/Product: carboxylesterase ES-3 #status predicted <MAI
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F;79,107,489/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;221,466/Active site: Ser, His #status predicted
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R;Medda, S.; Proia, R.L.
Eur. J. Biochem. 206, 801-806, 1992
Eur. J. Biochem. 206, 801-806, 1992
A;Title: The carboxylesterase family exhibits C-terminal sequence
A;Reference number: S23460; MUID:92299008; PMID:1606962
A;Accession: S23462
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A;Residues: 1-561 <ROB>
A;Cross-references: UNIPROT:Q63108; GB:X81395; NID:g550146; PIDN:CAA57158.1; PID:g55014
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578

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Carboxylesterase (EC 3.1.1.1) ES-10 precursor, microsomal - rat N;Alternate names: hydrolase A C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change 09-C;Accession: S10367; S12468; S51202; S23460; S14361 R;Robbi, M; Beaufay, H.; Octave, J.N.

Biochem. J. 269, 451-458, 1990 A;Fitle: Nucleotide sequence of CDNA coding for rat liver pI 6.1 es A;Reference number: S10367; MUID:90351366; PMID:2386485 A;Robbi. S10367 MUID:90351366; PMID:2386485 A;Rocession: S10367 MUID:90351366; PMID:2386485 A;Rostaidues: 1-565 - ROBIL A;Residues: 1-565 - ROBIL A;Residues: 1-565 - ROBIL A;Robbi. M. St. Toronto Fig. 4 is inconsistent with that from Fig. Ribbii. M. St. Toronto Fig. 4 is inconsistent with that from Fig.
                                 A;Molecule type: mRNA
A;Rosidues: 1-185,'Q',187-422,'M',424-505,'N',507-565 <MED>
A;Cross-references: EMBL:X65296; NID:957553; PIDN:CAA46391.1;
A;Cross-references: EMBL:X65296; NID:957553; PIDN:CAA46391.1;
R;Gaustad, R.; Sletten, K.; Lovhaug, D.; Fonnum, F.
Biochem. J. 274, 693-697, 1991
Biochem. J. 274, 693-697, 1991
A;Title: Purification and characterization of carboxylesterase
A;Reference number: S14361; MUID:91190080; PMID:2012599
A;Accession: S14361
                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 19-26,'D',28-37 <GAU>
C;Superfamily: cholinesterase; ch
                                                                                                                                                           A;Reference number: $51202; MUID:95077430; PMID:7986098
A;Accession: $51202
A;Molecule type: protein
A;Residues: 19-48 <MOR>
R;Medda, S.; Proia, R.L.
Bur. J. Biochem. 206, 801-806, 1992
A;Title: The carboxylesterase family exhibits C-terminal
A;Reference number: $23460; MUID:92299008; PMID:1606962
A;Accession: $23460
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C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum; F;1-18/Domain: signal sequence #status predicted <SIG>F;19-565/Product: carboxylesterase #status predicted <MAT>F;50-551/Domain: cholinesterase homology <CHBS
F;79,489/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;221,466/Active site: Ser, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-023-515-1 (1-2158) x S10367 (1-565)
AlaLeuIleThrThrAspSerLysProIleAlaAsnLeu-----IleAlaThrLeuSer
                                   TACCTGGAGGCCCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGT
                                                                                                            CCCATGGCCAAAGGCTTATTCCACAAAGCCATCATGGAGAGTGGGGTGGCCCATCATCCCT
                                                                                                                                                                                                                        GinValAlaAlaLeuHisTrpValGlnAspAsnIleAlaAsnPheGlyGlyAsnProGly
                                                                                                                                                 SerValThrilePheGlyGluSerAlaGlyGlyPheSerValSerAlaLeuValLeuSer
                                                                                                                                                                                   TCTGTGACCATCTTTGGCGAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCT
                                                                                                                                                                                                                                                CAGGTGGCTGCTCTGTCCTGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGC
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                                                                          ProLeuAlaLysAsnLeuPheHisArgAlaIleSerGluSerGlyValValLeuThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProvalmetvalTrpIleHisGlyGlyGlyLeuValValGlyGlyAlaSerThrTyrAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGACTGCCTCTAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1143 CACGAGTGTGGCTTCCTGCTGCCTATGAAGGAGGCTCCTGAGATCCTCAGTGGC----- 1196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 ValSerArgSerHi8ArgAspAlaGlyAlaProThrPheMetTyrGluPheGluTyrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           391 GluLysMetIleProValValAlaGluLysTyrPheGlyGlyThrAspAspProAlaLys 410
       545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332 GluGluIleLeuAlaGluLysSerPheAsnThrValProTyrIleValGlyIleAsnLys 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               312
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LysGluSerTyrProPheLeuProThrValIleAspGlyValValLeuProLysThrPro 331
TrpSerGlu------LeuArgAlaLysGluAlaAlaGluFro 557
                                                                                                                                                                                         GlySerProAsnGlyGlyGlyLeuProHisTTpProGluTyrAspGlnLysGluGlyTyr 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProSerPheValSerAlaMetArgProLysThrValIleGlyAspHisGlyAspGluLeu 470
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                                                TGGACCAGCACCATCCCCCTGATCCTGTCTGCCTCCGACATGCTCCACAGTCCT 1781
                                                                                                                                          CTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTGGATTTT 1727
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LeuLysIleGlyAlaSerThrGlnAlaAlaGlnArgLeuLysAspLysGluValAlaPhe
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Search completed: June 15, 2005, 08:55:12 Job time: 72.97 secs

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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-QC/cgn2 1/USPTO spool/6664091/runat 14062005 133459 9335/app query.fasta 1.4238
-QB=UniFrot_03 -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN-2000000000
-USER=6664091 @CCM_1 389 @runat 14062005 133459 9335 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LOGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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[2] SEQUENCE FROM N.A. TISSUE=PCR rescued clones:	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		"Generation and initial analysis of more than 15,000 full-length human		A., Schein J	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	ia A.M., Gay	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	TISSUE=PCR rescued clones;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=9606;	Primates;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens (Human).	Name=FLJ31547;	otein.	(TrEMBLrel. 27, Last	(TrEMBLrel. 27,	05-JUL-2004 (TrEMBLrel. 27, Created)	Q6NT32 PRELIMINARY; PRT; 575 AA.	732 1

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US-10-023-515-1 (1-2158)
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
EMBL; BC069501; AAH69501.1; -.
HSSP; P12337; 1K4Y.
GO: GO:0003824; F:catalytic activity; IEA.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs.
Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.
PROSITE; PS00141; CARBOXYLESTERASE_B_2; 1.
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RA Wakamatsu A., Hayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Pujimori K.,
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RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Pujimori K.,
RA Kanehori K., Takahashi-Pujii A., Hara H., Tanase T., Nomura Y.,
RA Kanehori K., Youki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Mizushima-Sugamo J., Satoh T., Shirai Y., Nakagawa K.,
RA Mizushima-Sugamo J., Satoh T., Shirai Y., Nakagawa K.,
RA Mizushima-Sugamo J., Satoh T., Shirai Y., Nakagawa K.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
"COmpas H., Sada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
"Compas H., Sada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
"Compas H., Masaho Y., Yamashita R.,
"Compas and characterization of 21,243 full-length human terminal sugamo T., Nakagawa K.,
"Compas and characterization of 21,243 full-length human terminal sugamo S., Sasaki M.,
"Compas and the sugamo T., Maramura Y., Ohara O., Isogai T., Sugano 
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
X Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F. Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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RA Hopkins R.F., Jordan R., Bonaldo M.F., Casrainci P., Prange C.,
RA Hopkins R.F., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Kockwan J.J., McKernan K.J., Mak J.A., Gunaratne P. H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodargren B.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Hokesley R.W., Touchman J.W., Green B.D., Dickeon M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Hopkinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Hopkinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                   TISSUE=PCR rescued Strausberg R.;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Hypothetical protein FLJ31547.
SIMILARITY: Belongs to the type-B
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  GAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAATGCGTCAGACTCT
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Percent Similarity:
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Query Match:
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InterPro; IPR000379; Ser_estrs.
Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE B 1;
PROSITE; PS00941; CARBOXYLESTERASE B 2;
Hydrolase; Hypothetical protein.
SEQUENCE 525 AA; 58200 MW; 7724878B8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P12337; 1K4Y.
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                     CACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGAGGCCCATGATTAT
                                                                                                                                                             GTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGCGAG
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                                                                                   SerAlaGlyAlaIleSerValSerSerLeuIleLeuSerProMetAlaLysGlyLeuPhe
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Q8NBC8;
Q1-QCT-2002 (TremBirel 22, Created)
Q1-QCT-2003 (TremBirel 22, Last seq
Q1-QCT-2003 (TremBirel 25, Last ann
                 Hypothetical protein FLJ33678
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
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RA PubMedal4702039; DOI=10.1038/ng1285;
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Minomiya K., Ishibashi T., Yamashita H., Murakawa E., Omura Y.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Mono Y., Takahashi F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Kanehori K., Takahashi F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Yoshikawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H.,
RA Misagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H.,
RA Hishigaki H., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Morayama H., Satoh N., Tashiro H., Tanigami A., Fujiwara T.,
RA Oho T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Oho T., Yamada K., Mayahama H., Satoh S., Itoh T., Shigeta K., Senba T.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Okimura K., Nagase T., Nomura Y., Ohara O., Isogai T., Sasaki M.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Misai R., Vada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                       Nat. Genet. 36:40-45(2004).

-!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.

RMBL; AK09097; BAC03565.1; -.

GO; GO:0016787; F:hydrolase activity; IEA.

InterPro; IPR002018; CarbesteraseB.

InterPro; IPR002079; Ser estrs.

Pfam; PF00135; COesterase; 1.

PROSITE; PS00122; CARBOXYLESTERASE_B_2; 1.

PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
                                                                                                                                                                                                                                                                                                                                                                              Hydrolase.
SEQUENCE
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GACGTGCTGGTTGTGGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACCACATGG
                                                                                                   ATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTGAACATC
                                             GlyAlaPheLysThrGlySerAlaSerIlePheAspGlySerAlaLeuAlaAlaTyrGlu
                                                            GGTGCCTTCAAGACTGGCTCCATCTTTGATGGGTCCGCCCTGGCTGCCTATGAG
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                                                                                                                                                                                                                                                                    RA Miyazaki M., Yamashita T., Taira H., Suzuki A.;

RT "cauxin family protein.";

RT Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.

C -! - SIMILARITY: Belongs to the type-B carboxylesterase/lips

DR EMBL, halls6392; BAD35015.1; -.

DR GO; GO:0003824; F:catalytic activity; IEA.

InterPro; IPR002018; CarbesteraseB.

InterPro; IPR002018; Ser_estrs.

PR InterPro; IPR00379; Ser_estrs.

R Ffam; PF00135; COesterase; 1.

R PROSITE; PS0012; CARBOXYLESTERASE B 1; 1.

R PROSITE; PS00941; CARBOXYLESTERASE B-2; 1.

M Hydrolase.

O SEQUENCE 575 AA; 63620 MW; 1005C35E82E1183D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         Q6AW47 PRELIMINARY; PRT; 575 AA. Q6AW47; 25-OCT-2004 (TrEMBLrel. 28, Created) 25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Carboxylesterase-like urinary excreted protein.
                                                                                                                                                                                                                                                                                                                                                                                           Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
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86.75%
75.68%
58.11%
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Matches:
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carboxylesterase/lipase

Euteleostomi; Canis.

Gaps:

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              GCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGAGAAGTTACTG
                                                         ACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTTTCGGTGGT
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US-10-023-515-1 (1-2158) x Q6AW46
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A "Mayazaki M., Yamashita T., Taira H., Suzuki A.;

A "Jazaki M., Yamashita T., Taira H., Suzuki A.;

A "Jazaki M., Yamashita T., Taira H., Suzuki A.;

T "cauxin family protein.";

Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.

C -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase fam:

EMBL; AB186393; BAD35016.1; -.

EMBL; AB186393; BAD35016.1; -.

R GO; GO:0003824; F:catalytic accivity; IEA.

InterPro; IPR002018; CarbesteraseB.

InterPro; IPR00379; Ser_estrs.

InterPro; IPR00379; Ser_estrs.

Pfam; PF00115; COesterase; 1.

PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.

PROSITE; PS00121; CARBOXYLESTERASE_B_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation updat
Carboxylesterase-like urinary excreted protein.
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TrpIlePheGlyAlaIleIleGlu-----
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Sciurognathi; Muridae; Murinae; Mus
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TTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGGCCACGGAGGAGGAGAAGTTACTGAGC 1568
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C -|- SIMILARITY: Belongs to the type-B carboxylesterase/lipase fam
R EMBL; AB045377; BAC22577.1; -.

R HSSP; p12337; IK4Y.

R GO; GO:0016787; F:hydrolase activity; IEA.
R InterPro; IPR002018; CarbesteraseB.
R InterPro; IPR003079; Ser_estrs.
R Ffam; PF00135; COesterase; 1.

R PF0SITE; PS00122; CARBOXYLESTERASE_B 1; 1.
R PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.

W Hydrolase.
Q SEQUENCE 545 AA; 60505 MW; 9F73FA693D271FA9 CRC64;
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MEDLINE-2245814; PubMed=12401131; DOI=10.1042/BJ20021446;

Miyazaki M., Kamile K., Soeta S., Taira H., Yamashita T.;

"Molecular cloning and characterization of a novel carboxylesterase-
"Molecular cloning and characterization of a novel carboxylesterase-
like protein that is physiologically present at high concentrations of the urine of domestic cats (Felis catus).";
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Q81034;
Q81034;
Q81034;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Carboxylesterase-like urinary excreted protein.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae,
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                                                             argSerLeuAlaLeuTyrLeuValHisThrPheLeuAsnIleProThrGlnTyrLeuHis
                                                                     AAGTCCCTTGCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTGAGTATTTGCAC
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                                                                                                                                                                                                                     GATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAATGCGTCA
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TISSUE-Temporal lobe right;
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai Suzuki Y., Sugano S., Hashimoto K.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the type-B carboxylesterase/1
EMBL; AB068073; BAB46884.1; -.
HSSP; P12337; 1K4Y.
InterPro; IPR002018; CarbesteraseB.
Pfam; PF00135; COesterase; 1.
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SEQUENCE 361 AA; 41032 MW;
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                          SASB ANAPL STANDARD; PRT; 557 AA. 004791; 01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Patty acyl-CoA hydrolase precursor, medium chain (Thioesterase B).
Anas platyrhynchos (Domestic duck).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
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US-10-023-515-1 (1-2158) x SASB_ANAPL
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R PIR; A47162; A47162.

R HSSP; O77540; 1K4Y.

R InterPro; IPR0002018; CarbesteraseB.

R InterPro; IPR000379; Ser_estrs.

R InterPro; IPR000379; Ser_estrs.

R Ffam; PF00135; COesterase; 1.

DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.

DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.

PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hwang C.-S., Kolattukudy P.E.;

"Molecular cloning and sequencing of thioesterase B cDNA and

"Molecular cloning and sequencing of thioesterase B gene associated with

stimulation of expression of the thioesterase B gene associated with

hormonal induction of peroxisome proliferation.";

J. Biol. Chem. 268:14278-14284(1993).

-I-FUNCTION. Fatty acid biosynthesis chain termination and release of

the free fatty acid product is achieved by hydrolysis of the thio

ester by a thioesterase. This thioesterase may be associated with

peroxisome proliferation and may play a role in the production of

3-hydroxy fatty acid diester pheromones.

-I-TISSUE SPECIFICITY: Highest levels in uropygial gland, much lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE TISSUE=Uropygial gland; MEDLINE=93300823; PubMed=8314791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
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                                                                                                                                                                                                                        CAAGTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCTTTGCT
GATCAACACATGCTC
                                    ValArgAspAlaAlaSerTyrProProMetCysLeuGlnAspLys-----ValLeu
                                                                        TTGCGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTA 422
                                                                                                             LysProProValGlyProLeuArgPheSerGluProGlnProProGluProTrpLysGly 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fatty acyl-CoA hydrolase.
Acyl-ester intermediate (By similarity).
Charge relay system (By similarity).
Charge relay system (By similarity).
By similarity.
N-linked (GlcNAC. . .) (Potential).
; 03E35D90A037F6B0 CRC64;
                                                                                                                                                                                                                                                                                                                                  (1-557)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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GTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTGCTTTGAAGACACGAAGCCGGCTTTT
                                                                                                                 ProLeuPheValPheSerAlaValGluValAlaArgHisHisArgAspAlaGlyAsnPro
                                                                                                                                  GTGTTCTTTGTGGTCCCTGCACTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCT
                                                                                                                                                                                                                                                                                                                                                        CCTTCCATCATCGAGTCAATAACCACGAGTGTGGCTTCCTGCTGCCT---ATGAAGGAG 1175
                                                                                                                                                                         LeuAlaLeuSerPheLysGlyAlaProSerAspIleValAspLeuValTyrAsnGluTyr
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RP SEQUENCE FROM N.A.

RC STRAIN=TVB/N, TISSUB=Colon, and Kidney;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Heich F.R.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.R.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.R.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Rohas S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Rahes J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;
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               SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
Strausberg R.;
                                                                                         SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
Strausberg R.;
Submitted (MAR-2002) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q91WG0 PRELIMINARY, PKI; JOLIN.
Q91WG0;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Carboxylesterase 2 (Carboxylesterase ML3 precursor)
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Kidney;
                                                                                                                                                                                         Submitted (OCT-2001) to the
                                                                                                                                                                                                                                                                                                     Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Ces2; Synonyms=ces2A3; Mus musculus (Mouse).
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 (JUN-2002) to the
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LysLeuLysGluArgLysMetGluPheTrpMetGlnLeuThrGluGlnIleMetSerAsp
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Pred. No.:
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RX MEDININE=22744052; PubMed=12859986; DOI=10.1016/S0003-9861(03)00286-8;

RA Purihata T., Hosokawa M., Nakata F., Satoh T., Chiba K.;

RY "Purification, molecular cloning, and functional expression of rinducible mouse liver acylcarnitine hydrolase in C57BL/6 mouse, rounded by the carboxylesterase multigene family.";

RY belonging to the carboxylesterase multigene family.";

RY belonging to the carboxylesterase multigene family.";

RY belonging to the carboxylesterase multigene family.";

RY belonging to the type-B carboxylesterase/lipase family.

RY SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.

RY EMBL; BC015290; ARM15290.1; -.

RY EMBL; BC024178; ARM15170.1; -.

RY EMBL; BC034170; ARM31170.1; -.

RY EMBL; BC034178; ARM34178.1; -.

RYBL; BC034191; ARM34191.1; -.

RYBL; BC034191; ARM34191.1; -.

RYBL; ARM14180 ALM34191.1; -.

RYBL; ARM151 BAC78623.1; -.
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GO; GO:0005615; C:extracellular space; TAS
PÉam; PF00115; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE B_1; 1.
PROSITE; PS00941; CARBOXYLESTERASE B_2; 1.
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SEQUENCE FROM N.A.
STRAIN-FVB/N; TISSUE=Colon,
Strausberg R.;
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TTCCCAGGAGGTGCCTTCAAGACTGGCTCCAGCCTCCATCTTTGATGGGTCCGCCCTGGCT
                                                                   LeuAsnIleTyrThrProAlaHisAlaHisGluGlySerAsnLeuProValMetValTrp
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STRAIN=57BL/6J; TISSUE=Ovary and uterus;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs
prepare full-length cDNA libraries for rapid discovery of new
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                          the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based 60,770 full-length cDNAs.";
Nature 420:563-573(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QBBK48;
QBBK48;
QBBK48;
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
RIKEN full-length enriched library, clone:5031415919 product:similar
to CARBOXYLESTERASE (EC 3.1.1.1) (ALI-ESTERASE) (B-ESTERASE)
(MONOBUTYRASE) (COCAINE ESTERASE) (PROCAINE ESTERASE) (METHYLBUTYRASE)
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STRAIN-C57BL/6J; TISSUE=Ovary and uterus;
MEDLINE=2108560; PubMed=11217851; DOI=10.1038
RIKEN FANTOM Consortium;
"Functional annotation of a full-length mouse
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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STRAIN=C57BL/6J; TISSUE=Ovary
The FANTOM Consortium,
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STRAIN-C578L/6J; TISSUE-Ovary and uterus;
MEDLINE-99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 409:685-690(2001).
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Name=9030624L02Rik;
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; DOI=10.1038/35055500;
(RISA) system-384-format
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Best Local Similari
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RC STRAIN=TVB/N; TISSUB=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D. Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Scheetz T.E.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Moorley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Fahey J., Helton E., Ketteman M., Madan A., Kodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myere R.M., Butterfield Y.S.,
RA Jones S.T., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
A Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Kurihara C., Matsuyama T., Kondo S., Konno H., Kouda M., Koya S.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A Saito R., Saitoh H., Sakai C., Sakai K., Sakzume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                     Hydrolase
SEQUENCE
                                                                                                                                                                                No.:
                                                                                                                                                                                                                                                                                                                        HSSP; P12337; IK4Y.

MGD; MGI:2443170; 9030624L02Rik.

GO; GO:005615; C:extracellular space;

InterPro; IPR002018; CarbesteraseB.

InterPro; IPR000379; Ser_estrs.
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                                                                                                        Match:
                                                                                                                                                                                                                                                                       PROSITE; PS00122;
PROSITE; PS00941;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=FVB/
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"Generation and initial analysis of
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STRAIN=C57BL/6J; TISSUE=Ovary
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Genome Res.
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               186
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TE; PS00122; CARBOXYLESTERASE_B_1;
TE; PS00941; CARBOXYLESTERASE_B_2;
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(1-2158)
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Akimura T., A
Hanagaki T.,
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Matches:
Conservative:
Mismatches:
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GlyGlnAspSerAlaSerProlleArgAsnThrHisThrGlyGlnValArgGlySerLeu

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GO; GO:0004091; F:carboxylesterase activit
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000886; ER_target S.
InterPro; IPR000379; Ser_estre.
PROSITE; PS00122; CARBOXYLESTERASE B 2; 1.
PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.
PROSITE; PS0014; ER_TARGET; UNKNOWN_1.
Hydrolase; Signal.
SIGNAL 1 27
CHAIN 28 559
SEQUENCE 559 AA; 62126 MW; 5866804F9AA7
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O35533;
O1-JAN-1998 (TrEMBLrel. O5, Created)
O1-JAN-1998 (TrEMBLrel. O5, Last sequence update)
O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Carboxylesterase precursor (EC 3.1.1.1).
Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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                                                                                                                                                   STRAIN-Syrian golden; TISSUE-Liver; Sone T., Ishida Y., Takabatake E., Wang C., Is submitted (MAY-1995) to the EMBL/GenBank/DDBJ-!-SIMILARITY: Belongs to the type-B carboxyl EMBL; D50577; BAA23605.1; -.
                                                                                                                                                                                                                                                        "Microsomal amidases and carboxylesterases.";
(In) Guengerich F.P. (eds.);
COMPREHENSIVE TOXICOLOGY VOLUME 3, Biotransformation,
Pergamon, Oxford (1997).
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STRAIN=Syrian
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C.Y.;
   Potential.
carboxylesterase.
; 5B68D4F9A47C6AD8
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ank/DDBJ databases.
carboxylesterase/lipase
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Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-CT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male colon cDNA, RIKEN full-length enriched
Library, clone:9030624L02 product:similar to CARBOXYLESTERASE (BC
3.1.1.1) (ALI-ESTERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAINE ESTERASE)
(PROCAINE ESTERASE) (METHYLBUTYRASE).
                                                                   STRAIN=C57BL/6J; TISSUE=Colon; MEDLINE=9279253; PubMed=10349636; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA (Meth. Enzymol. 303:19-44(1999).
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Colon;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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DOI=10.1038/35055500;
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X MEDLINE-20530913, PubMed=11076861; DOI=10.1101/gr.152600;

X MSDLINE-20530913, PubMed=11076861; DOI=10.1101/gr.152600;

X Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

X Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

X Mani N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

X Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

X Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

X Yoneda Y., Inoue K., Togawa Y., Izawa M., Ohazaki Y., Matsura S., Kawai J.,

X Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,

X Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,

X Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

TRIKEN integrated sequence analysis (RISA) system-384-format

T sequencing pipeline with 384 multicapillary sequencer.";

R Genome Res. 10:1757-1771(2000).
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                                                                                                                                                                                                                                                     MGD; MGI:2443170; 9030624L02Rik.
GO; GO:0005615; C:extracellular space;
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs.
Pfam; PF00135; COesterase; 1.
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Nature 420:563-573(2002).
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                                                                                                                                                                                                        GlyGluSerAlaGlyGlyThrSerValSerSerHisValValSerProMetSerGlnGly
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||ThrArgLysThrLeuProAlaValLeu
                                                                                                           AspGluTyrGlyTrpIleLeuProThrIleMetAspProAlaGlnLysIleGluGluIle
                                                                                                                                            CACGAGTGTGGCTTCCTGCCTG-----
                                                                                                                                                                         GlnGluLeuMetAlaSerLysAspPheHisProValProSerIleIleGlyIleAsnAsn
                                                                                                                                                                                                                                       AsnSerGluThrLeuMetCysCysLeuArgGlyLysAsnGluAlaGluMetLeuAlaIle
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                                                                             -ATGAAGGAGGCTCCTGAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCCTCCATCTG
                                              LysSerThrAlaLeuLysMet 379
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XX MEDILINE-22388257; Pubmed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA RAHA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Fahey J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Arnan M., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (T)
05-JUL-2004 (T)
05-JUL-2004 (T)
Hypothetical p)
Name=BC015286;
      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q6PDB7;
                                                      Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STEPATN=FVB/N; TISSUE=Colon;
                                              mouse cDNA sequences.";
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation updat
protein BC015286.
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                               U.S.A.
                              99:16899-16903 (2002)
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Sciurognathi; Muridae; Murinae; Mus
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InterPro; IPR002018; CarbesteraseB.
InterPro; IPR00379; Ser_estrs.
Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.
PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.
Hydrolase; Hypothetical protein.
SEQUENCE 556 AA; 61927 MW; 58DE05A33C7
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase
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EMBL; BC058815; AAH58815.1;
HSSP; P12337; 1K4Y.
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AACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCCTGGGTCCAGAAGAACATCGAGTTC
                                                                                                                                                                           AsnTrpGlyPheLeuAspGlnValAlaAlaLeuArgTrpIleGlnGlnAsnIleAlaHis
                                                                                                                    IleGinTyrArgLeuGlyValLeuGlyPhePheSerThrGlyAspGinHisAlaArgGly
                                                                                                                                           GTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACCACATGGGATCAGCATGCTCCGGGG
                                                                                                                                                                                                                                        HisGluGlySerAsnLeuProValMetValTrpIleHisGlyGlyGlyLeuValAlaGly
                                                                                                                                                                                                                                                                    GATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTCCCAAGGAGGTGCCTTCAAGACTGGC
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1266.50
60.17%
47.07%
32.71%
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Matches:
Conservative:
Mismatches:
Indels:
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-LeuGlyValMetLysGluIleLysLeuLysLeu
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231 809 211 749 191 689 171 629 151 569 131 밁 S В S 음 성

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RESULT 14
Q6GM54
ID Q6GM5
AC Q6GM5
DT 05-JU
Q6GM54 PRELIMINARY;
Q6GM54;
05-JUL-2004 (TrEMBLrel. 27,
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                                                                                                                              AGCACCATCCCC------CTGATCCTGTCTGCCTCCGACATGCTCCACAGTCCTCTT
                                                                                                                                                              LeuAspThrGlnProAlaValGlyArgAlaLeuLysSerArgArgLeuGlnPheTrpThr
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GlyIleTyrGlyThrGluAspAlaArgProLeuLeuThrThrAsnTyrGlyGlnLeuLeu 음 성 g ঠ В ঠ 밁 S 문 중 유

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Query Match:
DB:
US-10-023-515-1 (1-2158) x Q6GM54
                                                              Percent Similarity:
Best Local Similarity:
                                                                                                             Pred. No.:
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,
RA Diacchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diacchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Holting M., Madan A., Young A.C., Shevchenko Y., Butfard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
Ind mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
LOC443703 protein (Fragment).
Name=LOC443703;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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NCBI_TaxID=8355;
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Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifto
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AlaLeuPro---PheValHisSerPheThrSerValValProPheIleMetGluGluTyr
      GAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAACATCCTGCAC
                                                                                               ATCCCGCCTCAGTATTTGCAC----
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-----IleSerGlyTyrArgGluGlyMetGluLysLysAspIleGlnSerIleLeuVal
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Sone T., Kunitomo T., Isobe M.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-i-SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
BMBL; AB010632; BAA25691.1; -.
HMBL; AB010632; BAA25691.1; -.
HSSP; P37967; IQB3.
GO; GO:0014091; F:carboxylesterase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR000379; Ser_estrs.
InterPro; IPR000379; Ser_estrs.
InterPro; IPR000379; Ser_estrs.
                                                                                                                                                                                                           CHAIN
SEQUENCE
                                                                                                                                                                                                                                                 Pfam; PF00135; COesterase; 1.

PROSITE; PS00122; CARBOXYLESTERASE B 1;
PROSITE; PS00941; CARBOXYLESTERASE B 2;
Hydrolase; Signal.

26 Potential.
SIGNAL 1 26
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O70177;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Carboxylesterase precursor (EC 3.1.1.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=carboxylesterase;
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                CAGAAAGCATTTAAAGCAATTCCTTCCATCATCGGAGTCAATAACCACGAGTGTGGGCTTC 1157
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ValValGlyMetAlaSerMetTyrAspGlySerLeuLeuThrValAsnGluAspLeuVal 173
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AlaHisAlaArgGluGlySerAsnLeuProValMetValTrpIleHisGlyGlyAlaLeu 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTGAACATCTATGCGCCT
-----LeuSerSerIleSerMetSerGluAspCysLeuTyrLeuAsnValTyrAlaPro
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ThrThrHisThrGlyGlnValGlnGlyLysLeuAspHisValLysAspThrLysAlaGly
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                                                                                               ThrValSerThrThrValAlaLysLeuSerGlyCysGluAlaMetAspSerGluAlaLeu
                                                                                                                                                                GACCTGCAG---GTGGTTGCACATTTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCCTG
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                 AGCACCATCCCC 1745
                                                          CTGGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGGTGGATTTTTGGACC 1733
                                                                                                                                                                                       ValPhe---GlySerPhePheSerGlyMetLysLeuAspPhe-----ThrGluGlu
LysThrLeuPro
                                            |||||| ::: ::::: ||||||
LeuAspThrHisProAlaValAspArgAlaLeuLysAlaArgArgLeuGlnPheTrpThr 541
                                                                                          ProAsnSerGluGlyLeuProTyrTrpProAlaLeuAspHisAspGluGlnTyrLeuGln
                                                                                                          GTGTTCGGTGCTGCCTGAAGGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAG
                                                                                                                                                                                                                                                                                    HisPheGlnArg---SerHisAlaProValTyrPheTyrGluPheGlnHisAlaProSer 445
                                                                                                                                                                                                                                                                                                             CGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTCGGCACCGGCCTCAG 1433
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Search completed: June 15, 2005, 08:52:45 Job time: 226.639 secs



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Result
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Maximum Match 100%
Listing first 45 summaries
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-Q=/Cg12 1/USPTO spool/664091/runat 14062005 133500 9360/app query.fasta 1.4238
-Q=/Cg12 1/USPTO spool/664091/runat 14062005 133500 9360/app query.fasta 1.4238
-DB=ISSUSED Patents AA -QPWT=fastan -SUFFIX=n2p.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bis -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORR=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEADS=15=500 -MINLEN=0 -MAXL=200000000
-USER=664091 @CGN 1 154 @runat 14062005 133500 9360 -NCPU=6 -ICPU=3 -NO.MAP
-LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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is derived by analysis of the total score distribution.
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Fgapop 6.0 , 1
Delop 6.0 , 1
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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                            APPLICANT: Danks, Mary K.

APPLICANT: Houghton, Peter J.

APPLICANT: Houghton, Peter J.

ITILE OF INVENTION: Compositions and Methods

ITILE OF INVENTION: Tumor Cells

ITILE OF INVENTION: Tumor Cells

CURRENT APPLICATION NUMBER: US/09/595,682B

CURRENT FILING DATE: 2000-01-16

PRIOR APPLICATION NUMBER: 60/075,258

PRIOR FILING DATE: 1998-02-19

PRIOR FILING DATE: 1999-02-12

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin Ver. 2.0

LENGTH: 559

TYPE: PAT

ORGANISM: Homo sapiens

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 Alignment Scores: Pred. No.: Score:
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 5000-10-08

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRANTSCH for Windows Version 4.0

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                                                            Alignment Scores:
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                                                                                                             TYPE: PRT
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US-10-023-515-1 (1-2158) x US-09-949-016-6426 (1-559)
         1173 GAGGETCCTGAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAAC 1232
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                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

IIILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS

IIILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
US-10-023-515-1 (1-2158) x US-09-949-016-9670 (1-577)
                                                Percent Similarity:
Best Local Similarity:
Query Match:
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; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-09-595-682B-21
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PRIOR FILING DATE: 1998-02-19
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Danks, Mary K.
APPLICANT: Potter, Philip M.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Tumor Cells
FILE REFERENCE: SU-0005
CURRENT APPLICATION NUMBER: US/09/595,682B
CURRENT FILING DATE: 2000-01-16
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                                                           LysAlaProAlaGluIleLeuAlaGluLysLysTyrAsnMetLeuProTyrMetValGly
                                                                                      AATGAGCCICTAGATCTAȚIGTCTCAGAAAGCATTTAAAGCAATTCCȚTCCATCATCGGA 1133
                                                                                                                    ThrGluGluGuLeumetGluvalThrLeuLysmetLysPheMetAlaLeuAspLeuVal 308
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APPLICANT: Reng, Paul C.C.

APPLICANT: Renff, Thomas G.

ITILE OF INVENTION: Engineering Plant Resistance to Pyridines via FILE OF INVENTION: Expression of Esterase Enzymes FILE REFERENCE: 38-21 (10551) R.LE3 Pyridine Tolerance CURRENT APPLICATION NUMBER: US/09/264,737A

CURRENT FILING DATE: 1999-03-09

EARLIER FILING DATE: 1998-03-10

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

IRMCTH. 666
                                                                                                                                                            ; LENGTH: 566
; TYPE: PRT
; ORGANISM: Rabbit
US-09-264-737-2
         US-10-023-515-1 (1-2158)
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Patent No. 6107549
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                                                        GlyAspProLysGluAsnThrAlaPheLeuThrThrValIleAspGlyValLeuLeuPro
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APPLICANT: Danks, Mary K.

APPLICANT: Potter, Philip M.

APPLICANT: Houghton, Peter J.

TITLE OF INVENTION: Compositions and Methods

TITLE OF INVENTION: Tumor Cells

FILE REFERENCE: SC-005

CURRENT APPLICATION NUMBER: US/09/595,682B

CURRENT FILING DATE: 2000-01-16

PRIOR APPLICATION NUMBER: 60/075,258

PRIOR APPLICATION NUMBER: 60/075,258

PRIOR APPLICATION NUMBER: PCT/US99/03171

PRIOR APPLICATION NUMBER: PCT/US99/03171

PRIOR FILING DATE: 1999-02-12

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                                                                                             US-09-595-682B-26
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 26, Application Patent No. 6800483 GENERAL INFORMATION:
                                                                                                           TYPE: PRT ORGANISM: Oryctolagus cuniculus
                                                                                                                                            ENGTH: 543
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; Patent No. 5817490
; GENERAL INFORMATION:
APPLICANT: Hubbs, John C.
TITLE OF INVENTION: Enzymatic Proceedings of INVENTION: Ascorbic Acid,
ITILE OF INVENTION: 2-Keto-L-Guloni
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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US-08-845-295A-2
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ZIP: 37662-5075

COMPUTER READABLE FORM;

MEDIUM TYPE: 3.5 inch disk

COMPUTER: IBM Compatible

OBERATING SYSTEM: Windows 95

SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA;

APPLICATION NUMBER: US/08/84

FILING DATE: 25-April-97
                                                                                                                                                                                                                                                                                      ADDRESSEE: Eastmar
STREET: P.O. Box 5
CITY: Kingsport
STATE: Tennessee
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     JMBER: US/08/845,295A
25-April-97
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Percent Similarity:
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Query Match:
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; TYPE: Amino Acid
; TOPOLOGY: Linear
; MOLECULE TYPE: protein
US-08-845-295A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-023-515-1 (1-2158) x US-08-845-295A-2 (1-584)
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Pred. No.:
Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,87;
PILING DATE: 17-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REGISTRATION NUMBER: 70432
TELECOMMUNICATION INFORMATION:
TELEPHONE: 423-229-6189
TELEFPAX: 423-229-1239
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INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 584 amino acid
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Matches:
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SerValThrValAlaArgGlnHisArgAspAlaGlyAlaProThrTyrMetTyrGluPhe
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Best Local Similarity:
Query Match:
DB:
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Patent No. 6022719
GENERAL INFORMATION:
APPLICANT: Hubbs, John C.
TITLE OF INVENTION: Enzymat
TITLE OF INVENTION: ASCORDS
TITLE OF INVENTION: 2-Keto-
                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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PRIOR APPLICATION NUMBER: US 60/017,879; 08/845,295

PILING DATE: 17-May-96; 25-April-97

ATTORNEY/AGENT INFORMATION:

NAME: Cheryl J. Tubach

REGISTRATION NUMBER: 38,346

REFERENCE/DOCKET NUMBER: 70432

TELECOMMUNICATION INFORMATION:

TELEPHONE: 423-229-6189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOPTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/140,93
FILING DATE: 27-August-98
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 423-229-1239
                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Li
                                                                                                                                                                                                                                                                                                                              No . :
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: Amino Acid
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MEDIUM TYPE: 3.5 inch
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ZIP: 37662-5075
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                                                                                                                                                                            GluLeuThrProvalAlaThr-----PheThrAspLysTyrLeuGlyGlyThrAspAsp
                                              TATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAGCAC-----
                                                                           LysSer------ProGlu
                                                                                                  GGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAG 1253
                                                                                                                            MetGlyPheProLeuSerGluGlyLysLeuAspGlnLysThrAlaThrSerLeuLeuTrp 394
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| GlyValLeuLeuProLysMetProGluGluTleLeuAlaGluLysAspPheThrPheAsn 354
                                                                                                                                                                                                                                                        GGTGCTTTCTTTCCTAATGAGCCTCTAGATCTATTGTCTCAGAAA-----GCATTTAAA 1112
                                                                                                                                                                                                                                                                                  ThrLeuAspPheHisGlyAspGlnArgGluSerHisProPheLeuProThrValValAsp
                                                                                                                                                                                                                                                                                                                                   CysLeuArgGlnLysSerGluAspGluLeuLeuAspLeuThrLeuLysMetLysPheLeu 314
                                                                                                                                                                                                                                                                                                                                                             TGCCTGAGGACAAAACCCTCCAAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTC
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                                                                                         COUNTRY: USA

ZIP: 37662-5075

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,661
FILING DATE: 03-Septmeber-98
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/017,879; 08/845,295
FILING DATE: 17-May-96; 25-April-97
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70432
TELEPHONE: 423-229-6189
TELEPHONE: 423-229-6189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09146661 Patent No. 6136575
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APPLICANT: Hubbs, John C.
TITLE OF INVENTION: BRZYM
TITLE OF INVENTION: ASCOT
                                       TELEFAX: 423-229-1239
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
  OLECULE TYPE:
              TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                           STATE: Tennessee
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                                        584 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                     Eastman
 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                     Chemical Company
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Best Local Similarity:
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TGCCTGAGGACAAAACCCTCCAAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTC 1043
                          GlnIleAlaValLeuAlaGlyCysLysThrThrThrSerAlaValPheThrPheValHis
                                                                               GTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACCACATGGGGATCAGCATGCTCCGGGG
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ValLysAsnThrThrSerTyrProProMetCysCysGlnAspProValValGluGlnMet
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                                                     CTGCAGGTGGTTGCACATTTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCCTGCTGAGG
                                                                                                         GAGAGTGGGGTGGCCATCATCCCTTACCTGGAGGCCCATGATTATGAGAAGAGTGAGGAC
                                                                                                                                                           AGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCCTTATTCCACAAAGCCATCATG
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54.39%
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Matches:
Conservative:
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RESULT 11
US-09-150-515-2
                                                                                  Sequence 2, Application US/09150515
Patent No. 6271006
GENERAL INFORMATION:
APPLICANT: Hubbs, John C.
TITLE OF INVENTION: Enzymatic Process for the Manufacture
TITLE OF INVENTION: Ascorbic Acid, 2-Ketc-L-Gulonic Acid,
NUMBER OF SEQUENCES: 3
                                                                         NUMBER OF SEQUENCES: 3
                      ADDRESSEE: Eastm
STREET: P.O. Box
CITY: Kingsport
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                                          E: Eastman C
P.O. Box 511
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Best Local Similarity:
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ZIP: 3762-5075
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/150,5
FILING DATE: 09-SEP-1998
CLASSIFICATION DATA:
APPLICATION UNMBER: US 60/017,
FILING DATE: 17-May-96; 25-Apr
APPLICATION NUMBER: US 60/017,
FILING DATE: 17-May-96; 25-Apr
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70432
TELEPHONE: 423-229-6189
TELEPHONE: 423-229-6189
TELEPAX: 423-229-1239
TELEPAX: 423-229-1239
TELEPAX: AT3-229-G189
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                                                                                                                                                                  ThrSerAspLeuPheThrAsnPheThrGlyLysGluArgLeuThrLeuGluPhe-----
TCCATCTTTGATGGGTCCGCCCTGGCTGCCTATGAGGAC-----GTGCTGGTTGTGGTC
                               ArgGlyArgLeubrovalMetValTrpIleHisGlyGlyGlyLeuValLeuGlyGlyAla
                                                               GGCTCCAAGCTCCCCGTCTTGGTGTGGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCC
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Matches:
Conservative:
Mismatches:
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TTCGAAGGAGCACGGAGGAGGAGGAGGTTACTGAGCCGGAAGATGATGAATACTGGGCT
                                         GlnTyrArgProSerPheSerSerAspLysPheThrLysProLysThrValIleGlyAsp
                                                                                                                                                  GluLeuThrProvalAlaThr-----PheThrAspLysTyrLeuGlyGlyThrAspAsp
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                                                                                                                          CGGCACCGGCCTCAGTGCTTTGAAGAC-----ACGAAGCCGGCTTTTGTCAAAGCCGAC
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores: Pred. No.:
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TYPE: PRT
ORGANISM: Rabbit
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                                                                                                                                                                              GAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGATCAA 428
                                                                                                                                                                                                                                    CCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTGCGA 368
|||||||||:::|||||| ;::
|LeuProValMetValTrpIleHisGlyGlyGlyLeuMetValGlyGlyAlaSerThrTyr 134
                            CTCCCCGTCTTGGTGGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTT 584
                                                       SerGluAspCysLeuTyrLeuAsnIleTyrThrProAlaAspLeuThrLysArgGlyArg 114
                                                                                  TCAGAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAG 524
                                                                                                            HisMetLeuSerGluLeuPheThrAsnArgLysGluAsnIleProLeuLysPhe-----
                                                                                                                                                                  AsnThrThrSerTyrProProMetCysSerSerAspAla------ValSerGly 76
                                                                                                                                                                                                                                                                                                                                 ProSerAlaPro---ProValValAspThrValLysGlyLysValLeuGlyLysPheVal
                                                                                                                                                                                                                        ProLeuGlySerLeuArgPheAlaProProGlnProAlaGluSerTrpSerHisValLys
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1034.50
55.05%
42.24%
26.72%
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US-10-023-515-1 (1-2158) x US-09-264-737-1 (1-539)
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Feng, Paul C.C.
APPLICANT: Ruff, Thomas G.
TITLE OF INVENTION: Engineering Plant Resistance to Pyridines
TITLE OF INVENTION: Expression of Esterase Enzymes
FILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance
CURRENT APPLICATION NUMBER: US/09/264,737A
CURRENT FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: 60/077,377
EARLIER FILING DATE: 1998-03-10
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LysGlyGluGluValAlaPheTrpAsnAspLeuLeu 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAGAACCGCGGGTGGATTTTTGGACCAGCACCATC 1742
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                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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71
176
73
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                                  CTGAAGGGGGACATTGTTATGTTCGAAGGAGGAGGAGGAGGAGGAGGAGGAGTTACTGAGCCGG 1571
                                                                                                                                                                       GlyAlaProThrTyrMetTyrGluTyrArgTyrArgProSerPheSerSerAspMetArg
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                                                                                     LeuAlaAspLeuLeuPheGlyValProSerValAsnValAlaArgHisHisArgAspAla
                                                                                                                                                                                                                                                                                                      CTTGGAGATGTGTTCTTTGTGGTCCCTGCACTGATCACAGCTCGATATCACAGAGATGCT 1391
                                                                                                                                                                                                                                                                                                                                                GluLysTyrLeuGlyGlyThrAspAspProValLysLysLysAspLeuPheLeuAspMet 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TyrProileValAsnValSerLysGluLeuThrProValAlaThr 373
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  ----GluGlyAlaThrGluGluGluIleLysLeuSerLys
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                     Score:
                                                                                                                                                                                                                                                     Alignment Scores:
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US-08-446-100-26
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                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: hum
                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: pro
HYPOTHETICAL: YES
ANTI-SENSE: YES
                                                                                                                                                                                                                                     No.:
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COUNTRY: US
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70. 6001625
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US-10-023-515-1 (1-2158) x US-08-446-100-26 (1-454)
                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks;
STREET: 9669 A Main S!
CITY: Fairfax
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMEUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 425-4250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 454 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: bro
1632 TCTCTGTGGCCAGCTTATAATCTGACTGAGCAGTACCTCCAGCTGGACTTGAACATGAGC 1691
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9669 A Main Street, P.O.
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1542 GCCACGGAGGAGGAGTTACTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCT 1601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101
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                                                                                                                                                                                                               ValLysLysLysAspLeuIleLeuAspLeuIleAlaAspValMetPheGlyValProSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGA 1541
                                                                                                                                                                      CACCGGCCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGAT 148
                                                                                                                                                                                                                                         ACTGAAATCCGAGACAGTCTTCTGGACTTGCTTGGAGATGTGTTCTTTGTGGTCCCTGCA 1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyGlnLeuAspGlnLysThrAlaMetSerLeuLeuGlySerProIleProLeuPheAla 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCC-----AACAAGTCCCTTGCCCTCCATCTGATACAAAAC-----ATCCTGCAC 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATAACCACGAGTGTGGCTTCCTGCTGCCTATGAAGGAGGCTCCTGAGATCCTCAGTGGC 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluGluGluLeuLeuGluThrThrLeuLysIleGlyAsnSerTyrLeuTrpThrTyrArg 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCTGAGGTGCCTGAGGACAAAACCC 100.
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                                      GluLeuPheSerValPheGlyAlaProPheLeuLys------GluGly 371
                                                                                                                             TyrArgProSerPheSerSerAspMetLysProLysThrValIleGlyAspHisGlyAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ThrProGluGluLeuGlnArgGluArgAsnPheHisThrValProTyrMetValGlyIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluThrGlnArgGluSerThrLeuLeuGlyThrValIleAspGlyMetLeuLeuLeuLys 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GlyCysLysThrThrSerAlaAlaMetValHisCysLeuArgGlnLysThr 177
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                             US-10-023-515-1 (1-2158) x US-08-446-100-28 (1-454)
                                                             Query Match:
DB:
                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-446-100-28
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                                                                                                                                                                                     US-08-446-100-28
                                                                                                                                                                                                                                                                                                                      TELEPHONE: (703) 425-4250
TELEPAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 28
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 28, Applicate Patent No. 6001625
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/446
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
                                                                                                                                       . No.:
                                                                                                                                                                                                                FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: YES ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Okeana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: br
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Fairfax
STATE: VA
                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 22031
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 468 GAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTC 527
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5. 6001625
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                                                                                                                                                                                                                                  N-terminal
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942.50
59.55%
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                                                                                        Length:
Matches:
Conservative:
Mismatches:
                                                                           Indels:
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1482 GAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGGACATTGTTATGTTCGAAGGA 1541
                                                                                                                                                  1362 CTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTCGG 1421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 GluThrGlnArgGluSerThrLeuLeuGlyThrVallleABpGlyMetLeuLeuLeuLys 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 ValLeuValLysLysGlyAspValLysProLeuAlaGluGlnIleAlaIleThrAla--- 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              768 TCTGTGACCATCTTTGGCGAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 GlnValAlaAlaLeuArgTrpValGlnAspAsnTleAlaSerPheGlyGlyAsnProGly 100
                                                                                 CACCGGCCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGAT 1481
                                                                                                                     ValLysLysAspLeuIleLeuAspLeuIleAlaAspValMetPheGlyvalProSer
                                                TyrArgProSerPheSerSerAspMetLysProLysThrValIleGlyAspHisGlyAsp 357
                                                                                                                                                                                                            ACTGAAATCCGAGACAGTCTTCTGGACTTGCTTGGAGATGTGTTCTTTGTGGTCCCTGCA 1361
                                                                                                                                                                                                                                                        ileAlaLysGluLeuIleProGluAlaThrGluLysTyrLeuGlyGlyThrAspAspThr
                                                                                                                                                                                                                                                                                          ATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAGCACTCCCTG 130:
                                                                                                                                                                                                                                                                                                                           GlyGlnLeuAspGlnLysThrAlaMetSerLeuLeuGlySerProIleProLeuPheAla 277
                                                                                                                                                                                                                                                                                                                                                           TCC-----AACAAGTCCCTTGCCCTCCATCTGATACAAAAC-----ATCCTGCAC 1241
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AsnLysGlnGluPheGlyTrpLeuIleProMetGlnLeuMetSerTyrProLeuSerGlu 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrProGluGluLeuGlnArgGluArgAsnPheHisThrValProTyrMetValGlyIle 237
                                                                                                                                                                                                                                                                                                                                                                                                                            AATAACCACGAGTGTGGCTTCCTGCTGCCTATGAAGGAGGCTCCTGAGATCCTCAGTGGC 1190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGTCCGCCCTGGCTGCCTATGAGGACGTGCTGGTTGTGGTCGTCCAGTACCGGCTAGGA 647
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                Query Match:
DB:
                                             Best Local Similarity:
                                                               Percent Similarity:
                                                                                   Score:
                                                                                                   Pred. No.:
                                                                                                                Alignment Scores:
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Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (703) 425-4250
TELEPAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS:
                                                                                                                                                             FRAGMENT TYPE: NORIGINAL SOURCE: ORGANISM: huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDAGE
STREET: 960_
CITY: Fairfax
STATE: VA
COUNTRY: US
7TP: 22031
7TP: 270ADAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                HYPOTHETICAL: YES
                                                                                                                                                                                                                                  TOPOLOGIE TYPE: pro
                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                  STRANDEDNESS: sing TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O.
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60016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          358 GluLeuPheSerValPheGlyAlaProPheLeuLy8-------GluGly 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATTTTTGGACCAGC 1736
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                                                                                                                                                                                                                                                                                                              454 amino acids
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                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              528 CCCGTCTTGGTGGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGAT 587
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                                   ThrProGluGluLeuGlnArgGluArgAsnPheHisThrValProTyrMetValGlyIle
                                                                                                                                                                                                                                                       GluThrGlnArgHisSerThrLeuLeuGlyThrValIleAspGlyMetLeuLeuLeuLys 217
:::||||||
TyrargProSerPheSerSerAspMetLysProLysThrValIleGlyAspHisGlyAsp
                                                                                                                                                                                                                                      TCCAAGGAGCTGCTGACCCTCAGCCAGAAA------
                                                                                                                                                                                                                                                                                                                                -----GlyCysLysThrThrSerAlaAlaMetValHisCysLeuArgGlnLysThr 177
                                                                                                                                                                                                                                                                                                                                                                                                                       CCCATGGCCAAAGGCTTATTCCACAAAGCCATCATGGAGAGTGGGGGTGGCCATCATCCCT 887
                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTGTGACCATCTTTGGCGAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCT 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATATTTGGTTTCTCACCACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAGCACTCCCTG 130:
                                                                                                                                               GlyGlnLeuAspGlnLysThrAlaMetSerLeuLeuGlySerProlleProLeuPheAla 277
                                                                                                                                                                TCC-----AACAAGTCCCTTGCCCTCCATCTGATACAAAAC-----ATCCTGCAC 1241
                                                                                                                                                                                                                                                                          TTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAACCC 1001
                                                                                                                                                                                                                                                                                                                                                                                                       ProLeuAlaLysAsnLeuPheHisArgAlaIleSerGluSerGlyValAlaLeuThrSer 140
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                                                      1662 CAGTACCTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTG 1721
432 AlaPheTrpThrAsn 436
                                       GCCACGGAGGAGAAGTTACTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCT 1601
                                                                                                                                                                   GluLeuPheSerValPheGlyAlaProPheLeuLys------------------GluGly 371
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Search completed: June 15, 2005, 08:57:14 Job time: 63.6132 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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-MODEL=frame+_n2p.model -DEV=xlh
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Ygapop 10:0 , Ygapext
Fgapop 6.0 , Fgapext
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Copyright (c) 1993 - 2005 Compugen Ltd.
/ Cym.2 6/ptodata/1/pubpaa/US09E PUBCOMB.pep: */cgm.2 6/ptodata/1/pubpaa/US09E PUBCOMB.pep: */cgm.2 6/ptodata/1/pubpaa/US09C PUBCOMB.pep: */cgm.2 6/ptodata/1/pubpaa/US09.NEW_PUB.pep: */cgm.2 6/ptodata/1/pubpaa/US10E PUBCOMB.pep: */cgm.2 6/ptodata/1/pubpaa/US10.NEW_PUB.pep: */cgm.2 6/pto
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1 US-10-023-515-2

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; Sequence 2, Application US/10023515
; Publication No. US20020182636A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-122001
; CURRENT APPLICATION NUMBER: US/10/023,515
; CURRENT APPLICATION NUMBER: 60/256,369
pRIOR APPLICATION NUMBER: 60/256,369
pRIOR APPLICATION NUMBER: 60/279,508
pRIOR APPLICATION NUMBER: 60/279,508
pRIOR FILING DATE: 2001-03-28
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
LENGTH: 581
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; ORGANISM: Homo
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Sequence 2, Application US/10674636

Publication No. US20040086922A1

GENERAL INFORMATION:

APPLICANT: Curtis, Rory A. J.

APPLICANT: Silos-Santiago, Inmaculada

TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE

TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF

FILE REFERENCE: 10448-122001

CURRENT APPLICATION NUMBER: US/10/674,636
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; PRIOR APPLICATION NUMBER: US/10/023,515
; PRIOR FILLING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/256,369
; PRIOR FILLING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/279,508
; PRIOR TILLING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: Karicheti, Venkateswariu
APPLICANT: Kijos-Santiso, Inmaculada
APPLICANT: Kliso-Santiso, Inmaculada
TITLE DE INVENTION:
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PRIOR FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 136
SOFTWARE: FastSEQ for Windows Version 4
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Publication No. US20040197825A1
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                         ProAlaLeuIleThrAlaArgTyrHisArgAspAlaGlyAlaProValTyrPheTyrGlu
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HAPPLICANY: GLEAN GROUP LIFILING OF INVESTIONS. NOVEL COMPOUNDS
FILE REFERENCE: GP50039
FILE REFERENCE: GP50039
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-19
PRIOR PELLING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR FILING DATE: 2000-10-09
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR FILING DATE: 2001-01-09
PRIOR PILING DATE: 2001-01-09
PRIOR PILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR PILING DATE: 2001-03-19
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US-10-451-168-91
; Sequence 91, Application US/10451168
; Publication No. US20040091969A1
; GENERAL INFORMATION:
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RESULT 5
US-10-433-256-10
Sequence 10, Application US/10433256
Publication No. US20040081980A1
GENERAL INFORMATION:
APPLICANT: SANJANWALA, Madhusudan M.; YAO, Monique G. APPLICANT: AU-YOUNG, Janice K.; BAUGHN, Mariah R. APPLICANT: LEE, Ernestine A.; DING, Li
APPLICANT: HAFALLA, April J.A.; TANG, Y. Tom
APPLICANT: LU, Dyung Aina M.; LAL, Preeti G.
APPLICANT: WARREN, Bridget A.; YANG, Junming
APPLICANT: GANDHI, Narinder K.; NGUYEN, Danniel B.
APPLICANT: GANDHI, Narinder K.; NGUYEN, Danniel B.
APPLICANT: ISON, Craig H.
APPLICANT: LSON, Craig H.
APPLICANT: APPLICATION NUMBER: US/10/433,256
CURRENT APPLICATION NUMBER: US/10/433,256
PRIOR APPLICATION NUMBER: US 60/254,308
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: US 60/254,308
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; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/257,713
; PRIOR FILING DATE: 2000-12-21
; PRIOR PILING DATE: 2001-01-01
; PRIOR FILING DATE: 2001-01-19
; PRIOR FILING DATE: 2001-02-02
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PERL PROGRAM
; SEQ ID NO 10
; LENGTH: 642
; TYPE: PRT
; ORGANISM: Homo mapiens
; PEATURE:
; NUMBER OF SEQ ID NO 50/266,020
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; OTHER INFORMATION: Incyte ID No: 6538080CD1
US-10-433-256-10
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                                  CAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTG
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Matches:
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RESULT 6
US-10-451-168-92
; Sequence 92, Application US/10451168
; Publication No. US20040091989A1
; GENERAL INFORMATION:
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APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50039
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT APPLICATION NUMBER: DCT/US01/49232
PRIOR APPLICATION NUMBER: PCT/US01/49232
PRIOR FILING DATE: 2000-12-17
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR PRILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR APPLICATION NUMBER: 60/264,922
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PRIOR APPLICATION NUMBER: 60/264,922
PRIOR APPLICATION NUMBER: 60/264,928
PRIOR APPLICATION NUMBER: 60/264,935
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR APPLICATION NUMBER: 60/286,797
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PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 92
LENGTH: 581
TYPE: PRT
ORGANISM: Homo sapiens
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                                      ATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTCCCA
                                                                                         ProLeuGlySerLeuArgPheThrAsnProGlnProAlaSerProTrpAspAsnLeuArg
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 ${\tt GlyGlyAlaPheLysThrGlySerAlaSerIlePheAspGlySerAlaLeuAlaAlaTyr}$

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ACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTATGAGTTTTCGGCACCGG 1427
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APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZIKO
APPLICANT: ISHII, SHIZIKO
APPLICANT: HIO, YURI
APPLICANT: HIO, YURI
APPLICANT: HIO, YURI
APPLICANT: HIO, YURI
APPLICANT: HIO, YURI
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: NAGAHARI, KENUI
APPLICANT: NAGAHARI, KENUI
APPLICANT: NAGAHARI, KENUI
APPLICANT: NAGHON, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILIE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT APPLICATION NUMBER: 09/350,435
PRIOR APPLICATION NUMBER: 50/350,435
PRIOR FILING DATE: 2002-01-2
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 381
PRIOR APPLICATION NUMBER: 50/350,435
PRIOR FILING DATE: 2001-328381
PRIOR APPLICATION NUMBER: 50/350,435
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 381
SEQ ID NO 2375
LENGTH: 525
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APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
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CysGlyPheLeuLeuProMetValArgIleLeuAlaValHisThrAlaThrProSerAsn

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GlualaLeuLeuArgCysLeuArgThrLysProSerLysGluLeuLeuThrLeuSerGln

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GAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAATGCGTCAGACTCT

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1268 385	1209 CTTGCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAGTATTTGCACCTTGTG
1208 365	1149 TGTGGCTTCCTGCTGCCTATGAAGGAGGCTCCTGAGATCCTCAGTGGCTCCAACAAGTCC
1148 345	1089 CTATTGTCTCAGAAAGCATTTAAAGCAATTCCTTCCATCATCGGAGTCAATAACCACGAG
1088 325	29 AAAACAAAGICTTTTCACTCGAGTGGTTGATGGTGCTTTCTTTCCTAATGAGCCTCTAGAT
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968 285	09 GAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAATGCGTCAGACTCT
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848 245	89 TCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTATTC
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728 205	69 TGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCCTGG
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Percent Similarity:
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Query Match:
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; ORGANISM: Homo
US-10-114-270-196
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PRIOR FILING DATE: 2001-04-05
PRIOR PRILING DATE: 2001-04-06
PRIOR PILLING DATE: 2001-04-06
PRIOR PILLING DATE: 2001-04-06
PRIOR PRIOR PILLING DATE: 2001-04-10
PRIOR PPLICATION NUMBER: 60/282,930
PRIOR PPLICATION NUMBER: 60/282,934
PRIOR PILLING DATE: 2001-04-10
PRIOR PILLING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/283,512
PRIOR APPLICATION NUMBER: 60/283,710
PRIOR PILLING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR PILLING DATE: 2001-04-13
PRIOR PILLING DATE: 2001-04-17
Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 470
SEQ ID NO 196
LENGTH: 581
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                    TGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGC
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Sequence 2, Application US/10381898
Publication No. US20040086887A1
GENERAL INFORMATION:
APPLICANT: AZIMZAI, Yalda; BAUGHN,
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                                                        ValTrpValThrGlyTyrPro
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DB:

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APPLICANT: BOROWSKY, MARK L., DING, Li;
APPLICANT: DUGGAN, Brendan; ELLIOTT, Vicki S.;
APPLICANT: GANDHI, Ameena R.; GRIFFIN, Jennifer A.;
APPLICANT: HEALIA, April J.A.; ISON, Craig H.;
APPLICANT: KHAN, Farrah A.; LAL, Preeti G.;
APPLICANT: KHAN, Farrah A.; LAL, Preeti G.;
APPLICANT: RAMKIMAR, Jayalaxmi; RING, Huijun Z.;
APPLICANT: TANG, Y. Tom; TRIBOULEY, Catherine M.;
APPLICANT: YANG, Junming; YAO, Monique; YUE, Henry
TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
FILE REFERENCE: P1 0-23 USN
CURRENT FILING DATE: 2001-92 MONIQUE; YUE, Henry
FILOR APPLICATION NUMBER: US 0/236,947
PRIOR APPLICATION NUMBER: US 0/236,947
PRIOR FILING DATE: 2001-92
PRIOR APPLICATION NUMBER: US 60/236,947
PRIOR APPLICATION NUMBER: US 60/238,864
PRIOR APPLICATION NUMBER: US 60/242,323
PRIOR APPLICATION NUMBER: US 60/247,581
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Sequence 2219, Application US/10104047

Sequence 2219, Application US/20104047

Publication No. US20030236392A1

GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE

ITILE OF INVENTION: No. US20030236392A1e1 full length cDN:
FILE REFERENCE: H1-A0105

CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT FILING DATE: 2002-03-25

PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2219

TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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                                    TATGCGCCTGCCCACGCCGATACAGGCTCCCAAGCTCCCCGTCTTGGTGTTGGTTCCCAGGA 551
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Conservative:
Mismatches:
Indels:
Gaps:
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Sequence 2, Application US/10233933A
Publication No. US20040214171A1
GENERAL INFORMATION:
APPLICANT: Yamashita, Tetsuro
APPLICANT: Miyazaki, Masao
TITLE OF INVENTION: CAT KIDNEY DISE
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                                                                                                     LeuSerAlaSerAspMetLeuHisSerProLeuSerSerLeuThrPheLeuSerLeuLeu
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; PILE REFERENCE: SHIG FFUZUSTVO
; CURRENT APPLICATION NUMBER: US/10/233,933A
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: JP2002-057908
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 4
; SOFTMARE: PATENTIN Ver. 2.0
; SEQ ID NO 2
; SEQ ID NO 2
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                                                                                                            GAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTA
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                                     APPLICANT: Yamashita, Tetsuro
APPLICANT: Miyazaki, Masao
ITILE DE INVENTION: CAT KIDNEY DISEASE MARKER
FILE REPERENCE: SHIG FP02US006
CURRENT APPLICATION NUMBER: US/10/233,933A
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: JP2002-057908
PRIOR APPLICATION NUMBER: JP2002-057908
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 4
SOPTWARE: PATENTIN VEY: 2.0
SEQ ID NO 4
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                                                                                                                                                                                     Sequence 4, Application US/10233933A Publication No. US20040214171A1 GENERAL INFORMATION:
               LENGTH: 54
 ORGANISM: Felis catus
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US-10-023-515-1 (1-2158) x US-10-233-933A-4 (1-542)
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APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM p.1.c.
APPLICANT: GLAXO GROUP LIMITED
ITILE OF INVENTION. NOVEL COMPOUNDS
FILE REFERENCE: GP50039
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: DCT/US01/49232
PRIOR APPLICATION NUMBER: DCZ-66,710
PRIOR FILING DATE: 2000-12-17
PRIOR PILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR PILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR PILING DATE: 2001-03-19
PRIOR PILING DATE: 2001-03-19
PRIOR PILING DATE: 2001-03-19
PRIOR PILING DATE: 2001-04-04
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Publication No. US20040091969A1
GENERAL INFORMATION:
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SOFTWARE: PastSEQ for Windows Version
SEQ ID NO 93
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US-09-925-298-689
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Publication No. US20020039764A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapie
FEATURE:
NAME/KEY: SITE
LOCATION: (1)
OTHER INFORMATION: X
NAME/KEY: SITE
LOCATION: (7)
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TYPE: PRT
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                                               411 TGGCTGCTCTTAGATCAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAA 470
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ArgAspGlyThrThrHisProAlaMetCysLeuGlnAspLeuThrAlaValGluSerGlu
                                                                                            CGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAAC--------
                                                                                                                    GTGGATTTTTGGACCAGCACCATCCCCCTGATCCTGTCTGCCTCCGACATGCTCCACAGT 1778
                        PheLeu-----SerGlnPheAsnMetThrPheProSerAspSerMetSerGlu
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                                                                                                                                                                                                                                                              388 GlyAspProGlnThrLeuGlnAlaGlnPheGlnGluMetMetAlaAspSerMetPhevai
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TTCGAAGGAGCCACGGAGGAGGAGGAAGTTACTGAGCCGGAAGATGATGAATACTGGGCT 1592
                                                   HisGlyAspGluLeuProPheValPhe---ArgSerPhePheGlyGlyAsnTyrIleLys 465
                                                                                 CACGCTGATGAAGTCCGCTTTGTGTTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATG 1532
                                                                                                                                                                                          IleProAlaLeuGlnValAlaHisPhe---GlnCysSerArgAlaProValTyrPheTyr 426
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|GluPheGlnHisGlnProSerTrpLeuLysAsnIleArgProProHisMetLysAlaAsp
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; Publication No. US20030054421A1
; GENERAL INFORMATION:
APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins and Ant FILE REFERENCE: PA103PLC1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR FILING DATE: 2001-09-10
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR APPLICATION NUMBER: AC0/124,270
; NUMBER OF SEQ ID NOMER: 846
; SOFTMARE: Patentin Ver. 2.0
; SEQ ID NO 689
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Homo sapiens
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LOCATION: (1)
OTHER INFORMATION: X
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                                    ArgAspGlyThrThrHisProAlaMetCysLeuGlnAspLeuThrAlaValGluSerGlu
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1472 446	CGAAGCCGGCTTTTGTCAAAGCCGAC
1412 426	TGCACCTGTCTACTTCTAT gAlaProValTyrPheTyr
1352 407	93 CACTCCCTGACTGAAATCCGAGACAGTCTTCTGGACTTGCTTG
1292 387	33 ATCCTGCACATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAG ::: :::
1232 367	\TCCTCAGTGGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAAC ;;; 3luMetAspArgGluAlaSerGlnAlaAlaLeuGlnLysMetLeuThr
1172 347	25 ATCATCGGAGTCAATAACCACGAGTGTGGCTTCCTGCTGCCTATGAAG ::: :: ::: 28 IleValGlyValAsnAsnAsnGluPheGlyTrpLeuIleProLysValMetArgIleTyr
1124 327	65 TTCTTTCCTAATGAGCCTCTAGATCTATTGTCTCAGAAAGCATTTAAAGCAATTCCTTCC
1064 307	05 AAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACTCGAGTGGTTGATGGTGCT ::: :::
1004 287	GTGCCTGAGGACAAAACCCTCC YCysLeuArgGlyLysSerLys
944 267	91 CTGGAGGCCCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTC
890 251 .	831 ATGGCCAAAGGCTTATTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTAC :::::::
830 231	771 GTGACCATCTTTGGCGAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCC
770 211	711 GTGGCTGCTCTGTCCTGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCT
710 191	GGACCAG uAspGln
650 171	591 TCCGCCCTGGCTGCCTATGAGGACGTGCTGGTTGTGGTCGTCCAGTACCGGCTAGGAATA
590 151	TGATGGG : rAspGly
530 131	71 GACTGCCTCTACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCC
111	SerGlnPheAsnMetThrPheProSerAspSerMetSerGlu

	523 HisargLeuGlnPheTrpLysLysAlaLeuPro 533	523	몽
	CCGCGGGTGATTTTTGGACCAGCACCATCCCC 1745	1713	Ş
522	503 GlnGluGlnTyrLeuGlnLeuAsnLeuGlnProAlaValGlyArgAlaLeuLysAla 522	503	몽
171;	1653 CTGACTGAGCAGTACCTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGAGACTCAAAGAA 1712	1653	Ş
502	483 AsnPheAlaArgAsnGlyAsnProAsnGlyGluGlyLeuProHisTrpProLeuPheAsp 502	483	DЪ
1652	1593 ACCTTTGCTCGAACCGGGAATCCTAATGGGAACGACCTCTCTCT	1593	Ą
482	PheThrGluGluGluGlnLeuSerArgLysMetMetLysTyrTrpAla 482	466	DЪ
1592	1533 TTCGAAGGAGCCACGGAGGAGAGAGATGCTTGAGCCGGAAGATGATGAAATACTGGGCT 1592	1533	Ş

Search completed: June 15, 2005, 09:36:39 Job time: 181.194 Becs

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| Gyn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
| Gyn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
| Gyn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
| Gyn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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US-10-674-636-3
; Sequence 3, Application US/10674636
; Publication No. US20040086922A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
; TITLE OF INVENTION: FAMILY MEWHER AND USES THEREOF
; FILE REFERENCE: 10448-122001
; CURRENT APPLICATION NUMBER: US/10/674,636
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/10/023,515
; PRIOR APPLICATION NUMBER: 00/256,369
; PRIOR FILING DATE: 2000-12-18
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; PRIOR APPLICATION NUMBER: 60/279,508
; PRIOR APPLICATION NUMBER: 60/279,508
; PRIOR APPLICATION NUMBER: 60/279,508
; PRIOR APPLICATION NUMBER: 60/279,508
; PRIOR FILING DATE: 2000-03-28
; NUMBER OP SEQ ID NOS: 6
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1746
; ORGANISM: Homo sapiens
                                                              US-10-674-636-3
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                            APPLICANT: CITCLE, ROTY A. J.

APPLICANT: Silos-Santiago, Inmaculada

TITLE OF INVENTION: 53010, A MOVEL HUMAN CARBOXYLESTERASE

TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF

FILE REFERENCE: 10448-122001

CURRENT APPLICATION NUMBER: US/10/023,515

CURRENT FILING DATE: 2001-12-18

FRIOR APPLICATION NUMBER: 60/256,369

PRIOR FILING DATE: 2000-12-18

FRIOR APPLICATION NUMBER: 60/279,508

FRIOR APPLICATION NUMBER: 60/279,508

FRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1
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Publication No. US20020182636A1
GENERAL INFORMATION:
LENGTH: 2158
TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 1, Application US/10674636
Publication No. US20040086922A1
GENERAL INFORMATION:
APPLICANT: Curtis, Rory A. J.
APPLICANT: Silos-Santiago, Inmaculada
ITILE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
ITILE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-122001
CURRENT APPLICATION NUMBER: US/10/674,636
CURRENT FILING DATE: 2003-09-29
PRIOR APPLICATION NUMBER: US/10/023,515
PRIOR APPLICATION NUMBER: 05/256,369
PRIOR APPLICATION NUMBER: 60/256,369
PRIOR APPLICATION NUMBER: 60/256,369
PRIOR FILING DATE: 2000-12-18
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; PRIOR APPLICATION NUMBER: 60/279; PRIOR FILING DATE: 2001-03-28; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ FOR WINDOWS V6; SEQ ID NO 1
; LENGTH: 2158
; TYPE: DNA
; ORGANISM: Homo sapiens
; PEATURE:
; NAME/KEY: CDS
; LOCATION: (96)...(1838)
US-10-674-636-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1746; Conservative (
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US-10-757-262-45; Sequence 45, Application US/10757262; Publication No. US20040197825A1; GENERAL INFORMATION:
APPLICANT: Karicheti, Venkateswarlu; APPLICANT: Silos-Santiago, Inmaculada; APPLICANT: Eliasof, Scott D.
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TITLE OF INVENTION: METHODS AND COMPOSITIONS TITLE OF INVENTION: UROLOGICAL DISORDERS US: TITLE OF INVENTION: 1405, 636, 4421, 5410, 7111  
FOR INVENTION: 33751, 52872, 14063, 207  
TITLE OF INVENTION: 33751, 52872, 14063, 207  
TITLE OF INVENTION: 33951, 52872, 14063, 207  
TITLE OF INVENTION: 32720, 4809, 14303, 1620;  
TITLE OF INVENTION: 2543, 9626, 13231, 1620;  
TITLE OF INVENTION: 2543, 9626, 13231, 1620;  
TITLE OF INVENTION: 2543, 9626, 13231, 3240;  
TITLE OF INVENTION: 2543, 9626, 13231, 3240;  
TITLE OF INVENTION: 25053  
FILE REFERENCE: MPIO3-007PIRNOMNIM CURRENT FILING DATE: 2003-01-15  
PRIOR APPLICATION NUMBER: US 60/444,783  
PRIOR APPLICATION NUMBER: US 60/444,783  
PRIOR APPLICATION NUMBER: US 60/457,901  
PRIOR APPLICATION NUMBER: US 60/457,901  
PRIOR FILING DATE: 2003-02-04  
PRIOR FILING DATE: 2003-05-08  
PRIOR APPLICATION NUMBER: US 60/471,614  
PRIOR APPLICATION NUMBER: US 60/471,742  
PRIOR APPLICATION NUMBER: US 60/491,156  
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (96)...(1841)
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OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
OF INVENTION: 1305, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52308, 69112, 14930,
OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
OF INVENTION: 32720, 4809, 14303, 16565, 17827, 32620, 577, 619, 1423,
OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21655, 30911, 41897, 1643,
OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
OF INVENTION: 55053
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FITTLE OF INVENTION: MOVEE FILE REFERENCE: GP50039

CURRENT FILING DATE: 2003-11-12

PRIOR APPLICATION NUMBER: PCT/US01/49232

PRIOR RILING DATE: 2000-12-17

PRIOR APPLICATION NUMBER: 60/256,710

PRIOR RILING DATE: 2000-12-17

PRIOR APPLICATION NUMBER: 60/257,048

PRIOR PILING DATE: 2000-12-20

PRIOR PILING DATE: 2000-12-20

PRIOR PILING DATE: 2001-01-09

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: 60/266,797

PRIOR PILING DATE: 2001-02-06

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PRIOR PILING DATE: 2001-03-19

PRIOR PILING DATE: 2001-03-19

PRIOR PILING DATE: 2001-04-04

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PRIOR PILING DATE: 2001-06-28

NUMBER OF SEQ ID NOS: 110

SOFTWARE: PASTSEQ for Windows Version 4.0

SEQ ID NO 40

LENGTH: 1728

TYPE: DNA

ORGANISM: Homo sapiens
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                    GTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCCTTTGCTGCT
                                                          GTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCTTTGCTGCT
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RESULT 8 US-10-104-047-249 Sequence 249, Application US/10104047 Publication No. US20030236392A1 GENERAL INFORMATION: APPLICATION: APPLICATION: FILE REFERENCE: H1-A0105 CURRENT APPLICATION NUMBER: FILE REFERENCE: H1-A0105 CURRENT PLING DATE: 2002-03-25 PRIOR PILING DATE: 2002 TYPE: DNA DRANLISM: Homo sapiens US-10-104-047-249 Query Match Best Local Similarity 99.2*; Pred. No. 0; Best Local Similarity 99.2*; Pred. No. 0; Matches 1653; Conservative 0; Mismatches 3; Indels 10; Gaps 1; Matches 1653; Conservative 0; Mismatches 1611	1641 CACCATCCCCTGATCCTGCCTCCCACATCTCCTCCATTCTTCCTTAAC 1700	1521 TAATGGGAACGACCTGTCTCTGTGGCCAGCTTATAATCTGACCAGCAGTACCTCCAGCT 1580		1281 ATATCACAGAGATGCTGCTACCTGTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTG 1340	CTCCAACAAGTCCCTTGCCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAGTA
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RESULT 9

US-10-114-270-195

Sequence 195, Application US/10114270

Publication No. US20040030110A1

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DF INVENTION: NO. US20040030110A1el Pr
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PRIOR PILING DATE: 2001-04-10
PRIOR PILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/283,710
PRIOR PILING DATE: 2001-04-13
PRIOR PILING DATE: 2001-04-17
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Remaining Prior Application data removed - See File Wrapper or PALM.
PRIOR PILING DATE: 2001-04-17
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PRIOR APPLICATION NUMBER: 60/283,512
PRIOR APPLICATION NUMBER: 60/283,710
PRIOR PILLING DATE: 2001-04-12
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Best Local Similarity 95.3%;
Matches 1496; Conservative
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CURRENT APPLICATION NUMBER: US/10/114,270
CURRENT FILING DATE: 2002-11-27
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                                                                   AGCCACGGAGGAGAAGTTACTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGC
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PRIOR APPLICATION NUMBER: 2003-11-12

PRIOR APPLICATION NUMBER: PCT/US01/49232

PRIOR FILING DATE: 2000-12-17

PRIOR APPLICATION NUMBER: 60/256,710

PRIOR FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: 60/257,048

PRIOR APPLICATION NUMBER: 60/260,482

PRIOR APPLICATION NUMBER: 60/260,482

PRIOR PILING DATE: 2001-^^
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PRIOR PRIOR PAPELICATION NUMBER: 60/264,922
PRIOR PRIOR PAPELICATION NUMBER: 60/266,797
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR PRIOR PRIOR DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR PILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/289,622
PRIOR PILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 110
SOPTWARE: FRANCSEQ for Windows Version 4
SEQ ID NO 41
LENGTH: 1746
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity 95.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 1494;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: GP50039
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
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                       TACCTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGAGAGAT
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SOFTWARE: PERL Program

SEQ ID NO 20

LENGTH: 1857

TYPE: DNA
ORGANISM: Homo Bapiens
PEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 7473645CB1
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APPLICANT: BOROWSKY, Mark L.; DING, Li;
APPLICANT: BOROWSKY, Mark L.; DING, Li;
APPLICANT: DUGGAN, Brendan; ELLIOTT, Vicki S.;
APPLICANT: DUGGAN, Brendan; ELLIOTT, Vicki S.;
APPLICANT: HAFALIA, April J.A.; ISON, Craig H.;
APPLICANT: HAFALIA, April J.A.; ISON, Craig H.;
APPLICANT: KHAN, Farrah A.; LiL, Preeti G.;
APPLICANT: ARVIZU, Chandra S.; POLICKY, Jennifer L.;
APPLICANT: RAMKUMAR, Jayalaxmi; RING, Huijun Z.;
APPLICANT: RAMKUMAR, Jayalaxmi; RING, Huijun Z.;
APPLICANT: WARREN, Bridget; XU, Yuming;
APPLICANT: WARREN, Bridget; XU, Yuming;
APPLICANT: WARREN, Bridget; XU, Yuming;
APPLICANT: WARREN, Bridget; XU, Yuming;
APPLICANT: YANG, Yuming; YAO, Monique; YUE, Henry
TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
FILE REFERENCE: PI-0233 USN
CURRENT APPLICATION NUMBER: US/10/381,898
CURRENT APPLICATION NUMBER: US/0/380,864
PRIOR APPLICATION NUMBER: US 60/236,947
PRIOR APPLICATION NUMBER: US 60/238,864
PRIOR APPLICATION NUMBER: US 60/242,323
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/247,581
PRIOR APPLICATION NUMBER: US 60/247,581
PRIOR APPLICATION NUMBER: US 60/249,519
PRIOR APPLICATION NUMBER: US 60/249,519
PRIOR APPLICATION NUMBER: US 60/252,834
PRIOR FILING DATE: 2000-11-26
PRIOR APPLICATION NUMBER: US 60/252,834
PRIOR FILING DATE: 2000-11-26
PRIOR APPLICATION NUMBER: US 60/252,834
PRIOR FILING DATE: 2000-11-30
NUMBER OF SECTION SINGER: US 60/250,567
PRIOR APPLICATION NUMBER: US 60/250,567
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US-10-381-898-20
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Best Local Similarity 94.7%;
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; Pred. No. 0; 
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APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: MAGHARI, KENJI
APPLICANT: MAGHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR APPLICATION NUMBER: 40/350,435
PRIOR APPLICATION NUMBER: 3001-09-14
NUMBER OF SEG ID NOS: 3381
SOFTWARE: PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENT PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATE
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Publication No. US20030219741A1
GENERAL INFORMATION:
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Best Local Similarity 90.9%;
Matches 1505; Conservative
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ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
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OTSUKI, TETSUJI
WAKAMATSU, AI
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APPLICANT: MANSHITA, Tetsuro
APPLICANT: MANSHITA, MASSA
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CURRENT FILING DATE: 2002-09-03
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 2145
TYPE: DNA
ORGANISM: Felis catus
FEATURE:
NAME/KEY: CDS
LOCATION: (175)..(1803)
FEATURE:
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Best Local Similarity
Matches 1329; Conserv
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; APPLICANT: Yamashita, Tetsuro
APPLICANT: Myazaki, Masao
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; SEQ ID NO 1
; SEQ ID NO 1
; LENCTH: 1629
; TYPE: DNA
; ORGANISM: Felis Catus
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TITLE OF INVERVION: NOVEL COMPOUNDS
FILE REFERENCE: GS-50039
CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-17
PRIOR PPLICATION NUMBER: 60/257,048
PRIOR PRIOR PRIOR PRIOR OF STATE 2000-12-19
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR PILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR PILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR PILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR APPLICATION NUMBER: 60/289,622
PRIOR PILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 60/289,622
PRIOR FILING DATE: 2002-06-28
NUMBER: 0F SEQ ID NOS: 110
SOFTWARE: FASTSEQ FOR Windows Version 4.0
SEQ ID NO 42
LENGTH: 1071
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-451-168-42
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US-10-451-168-42
; Sequence 42, Application US/10451168
; Publication No. US20040091969A1
; GENERAL INFORMATION:
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Best Local Similarity 99.9%;
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APPLICANT: SMITHKLINB BEECHAM p.l.c.
APPLICANT: GLAXO GROUP LIMITED
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Listing first 45 summaries
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241	181	181	121	121	61	61			Query Match Best Local Similarity 100 Matches 1746; Conservative	-	source		-				MOTOM	S					
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CCTGGG	CCCCT	ICCCCT	TCAGG	TCAGG	AGTGGG	AGTGGG	CITCAT	CTTCAT		i Action	= "unkn	Qualif:	-A 3 1	S1108-	5				53740		cent U		
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Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AX600126 Sequence 3 from Patent 1 AX600126 AX600126.1 GI:28400192 1746 bp from Patent W00250256. DNA linear PAT 14-FEB-2003

Curtis,R.A. and Silos-Santiago,I. 53010, a novel human carboxylesterase family member thereof

Patent: WO 0250256-A 3 27-JUN-2002; Millennium Pharmaceuticals, Inc. (US) Cocation/Qualifiers 1. .1746 /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

DB 6;

Length 1746;

181 AACGTGTTCCTCGGAGTCCCCTTTGCTGCTCCCCCGCTGGGATCCCTGCGATTTACGAAC CTGTTGGGACACAGACAGTGGGGAAAAACTGGGCCTTCTGCTGAAGGGCCACAGAGGAAC ATGCCACAGGGACTTACTTCATCTGCTTCACAATGGTGCTTTTTCCTGATTCTCCAGCCC accadecredearedatricadedecaadcaadreacrerededaadcccrerecereic ACCAGGCTGGGATGGATTCAGGGCAAGCAAGTCACTGTGCTGGGAAGCCCTGTGCCTGTG Score 1746; Pred. No. 0; O; Mismatches <u>,,</u> Indels <u>,,</u> Gaps 240 180 180 120 120 60 60

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-	781 GCCATCATCCCTTACCTGGAGGCCCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTT 840	<u> </u>
	721 CTTATACTGTCTCCCATGGCCAAAGGCTTATTCCACAAAGCCATCATGGAGAGTGGGGTG 780	B 8
1741 CCTTGA	661 GGGGACCCCAGCTCTGTGACCATCTTTGGCGAGTCCGCGGGAGCCATAAGTGTTTCTAGT 720	B 8
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1621	541 TACCGGCTAGGAATATTTGGTTTCTTCACCACATGGGATCAGCATGCTCCGGGGAACTGG 600	B 8
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                                                  CCTGCACTGATCACAGCTCGATATCACAGAGATGCTGGTGGACCTGTCTACTTCTATGAG 1320
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ORIGIN	CDS	JOURNAL FEATURES SOURCE	AUTHORS TITLE	SOURCE ORGANISM	RESULT 4 AX600124 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	Db 1	0у 1	ეხ 1	97	рь 1		Qy 1	Db 1	Ωγ 1		φ			В
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RESULT 5 EC069501 LOCUS DEFINITION ACCESSION VERSION VERSION ORGANISM REFERENCE AUTHORS	B Q B Q B Q B	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
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NIH-MGC Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Baylor Human Genome Sequencing Center
cDNA Library Preparation: Baylor Human Genome Sequencing Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome

Sequencing Center
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Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, &
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny,
A.N., Gibbs, R.A.
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Director MGC Project.
Direct Submission
Submitted (29-ApR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Query Match 94.6%; Score 1651.6; DB 6; Length 2232; Best Local Similarity 99.5%; Pred. No. 0; Matches 1657; Conservative 0; Mismatches 9; Indels 0; Gaps 0 97 81 GGGAAAAACTGGGCCTTCTGCTGAAGGGCCACAGAGGAACACCAGGCTGGGATGGAT	FEATURES Location/Qualifiers 1. 232 1. 232 Feature /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" /noTe="Incyte ID No: 6538080CB1" ORIGIN	Ring, H.Z., Lee, B.A., Ding, L., Hafalia, A.J., Tang, Y.T., Yue, H Tribouley, C.M., Lu, D.A., Lal, P.G., Warren, B.A., Yang, J., Walla, N.K., Nguyen, D.B., Gandhi, A.R. and Ison, C.H. Drug metabolizing enzymes Patent: WO 0246426-A 23 13-JUN-2002;	SS ESM	RESULT 6 AX477711 LOCUS AX477711 DEFINITION Sequence 23 from Patent WO0246426. ACCESSION AX477711 VERSION AX477711 OT: 22216866	1711 1813	1651 CTGATCCTGTCTGCCTCCGACATGCTCCACAGTCCTCTTTCCTTCTTAACTTTCCTCTCT 1	DD 1833 GROCIGICICIGIAGCONGLIFAIRMICIGROGRAGARGARCACCAGGRACIAGRAC 1832 QY 1591 ATGAGCCTCGGACAGAGACTCADAGAACCGCGGTGGATTTTTTGGACCAGCACCATCCCC 1650	1573 AGCCGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACCGGGAATCCTAATGGGAAC 1 1531 GACTGTCTCTGTGGCCAGCTTATAATCTGACCAGCAGTACCTCCAGCTGGACTTGAAC 1	GCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGAGGAGAAGTTACTG 1 AGCCGGAAGATGATGAAATACTGGGCTACCTTTTGCTCGAACCGGGAATCCTAATGGGAAC 1	ACGAAGCCGGCTITTGICAAAGCCGACCACGCIGAIGAAGICCGCTITGIGIICGGIGGI 13	1353 GHIGCIGGIGCACCIGICIACLICIA GAGIII CGGCACCGGCCICAGIGCIII GAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTTCGGTGGT	1291 GARGETGGTGCACCTGTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTGCTTTGAAGAC	1231 GACTTGCTTGGAGATGTGTTCTTTGTGGTCCCTGCACTGATCACAGGTCGATATCACAGA	OY 1171 GTGGCTAATGAATACTTCCATGACAAGCACTCCCTGACTGA
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Query Match 93.4%; Score 1631.2; DB 6; Length 2092; Best Local Similarity 99.3%; Pred. No. 0; Matches 1653; Conservative 0; Mismatches 3; Indels 10; Gaps 1; Matches 1653; Conservative 0; Mismatches 3; Indels 10; Gaps 1; Oy 91 GGGCCTTCTGGTGAAGGGCCACAGAGGGAACACCAGGCTGGGATGGAT	RES	AUTHORS Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J.I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R., Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and Masuho, Y. Masuho, Y. Masuho, Y. TITLE Full-length cDNA sequences JOURNAL Patent: Ep 1308459-A 249 07-MAY-2003; Helix Research Institute (JD) - Poorty Nam	ACCESSION AX746724 VERSION AX746724.1 GI:32130991 KEYWORDS . SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; REFERRNCE 1 REFERRNCE 1 REFERRNCE 1 REFERRNCE 1	RESULT 7 AX746724 LOCUS DEFINITION Sermonce 746 from 2092 bp mRNA linear PAT 20-JUN-2003		ACCATCCCCTGATCCTGTCTGCCTCCGACATGCTCCACAGTCCTCTTTCTT	GACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACACCGCGGGTGGATTTTTGGACCAG		<u> </u>	OY 1341 CTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACGCTGATGAGAGTCCGCTTTGT 1400	Db 1344 TTTGCACCTTGTGGCTAATGAATACTTCCATGACAAGCACTCCCTGACTGA
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Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Sekine, M., Obayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Kikkawa, E., Ohiba, Y., Ishida, K., Ishibashi, T., Yamashita, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, K., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takayuchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, R., Takae, S., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takaeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Sasaki, N., Aotsuka, S., Yoshikawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimiu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Goto, Y., Shimiu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashima, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Jikema, Y., Okamoto, S., Okitani, R., Kawakami, T.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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210 257 270 GTCACTGTGCTGGGAAGCCCCTGTGCCTGTGAACGTGTTCCCTCGGAGTCCCCCTTTGCTG

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Is logal, T. and Yamamoto, J.

Is logal, T. and Yamamoto, J.

Is pirect Submission

La Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

Construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.
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Nakajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togashi,T.,
Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J.,
Satoh,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K.,
Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R.,
Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.
Complete sequencing and characterization of 21,243 full-length
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Clone distribution: MGC clone distribution information can be found through the I.N.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK plate: 51 Row: k Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis. FEATURES Location/Qualifiers 12298 /organism="Homo sapiens"	COMMENT CONTACT: MGC help desk Email: cgapbs-romail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center Center Center Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.	SOURCE Homo sapiens (human) ORGANISM Homo sapiens Entaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2298) AUTHORS Strausberg,R. TITLE Direct Submission Submitted (01-NOV-2002) National Institutes of Health, Mammalian Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov	RESULT 9 BC039073 LOCUS BC039073 DEFINITION Homo sapiens, similar to carboxylesterase, clone IMAGE:5174937, ACCESSION BC039073 VERSION BC039073.1 GI:25058132	Qy 1641 CACCATCCCCCTGATCCTGTCTGCCTCGACAGGCCTCCACAGGTCCTCTTTACC 1700	Qy 1521 TAATGGGAACGACCTGTCTGTGGCCAGCTTATAATCTGACTGA	Qy 1341 CTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGT 1400

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/clone_Tib="NIH_MGC_115"
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Mammalia; Eutheria;
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        Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 02068579-A 18978 06-SEP-2002;
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                                                                                                CCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAATGC
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0; Mismatches
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Eukaryota; Metazoa; C
Mammalia; Eutheria; P
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Sequence 20 from Patent
AX958392
AX958392.1 GI:40879350
                                                                                                                             Similarity
                                GTTACTGAGCCGGAAGATGATGATACTGGGCTACCTTTGCTCGAACCGGGA 1516
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nilarity 94.7%;
Conservative
                                                                                                                                                                                           organism="Homo sapiens"

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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                     ; Chordata; ; Primates;
                                                                                                        Score 1386.2;
Pred. No. 0;
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WO0226988.
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Catarrhini; Hominidae
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Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Petters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Hillyk, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hillyk, S.W., Villaion, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) REFERENCE Chases 1 to 1896) Strausberg, R. JUTYORS Strausberg, R. Direct Submission Submitted (29-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Baylor Human Genome Sequencing Center	RESULT 12 BC069548 LOCUS BC069548 LOCUS Homo sapiens hypothetical protein FLJ31547, mRNA (cDNA clone MGC:97193 IMAGE:7262439), complete cds. ACCESSION BC069548 VERSION WGC. SCURCE ORGANISH Homo sapiens (human) CRGANISH Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE AUTHORS Klausner, R.D., Collins, F.S., Wagner, L., Schuefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scheeft, T. R. Brownstein M. J. Hodin, T. R. Casavant, T.L., Cabeat, T. R. Brownstein M. J. Hodin, T. R. Casavant, T.L., Cabeat, T. R. Brownstein M. J. Hodin, T. R. Casavant, T.L., Cabeat, T. R. Brownstein M. J. Hodin, T. R. Casavant, T.L., Cabeat, T. R. Brownstein M. J. Hodin, T. R. Casavant, T.L., Cabeat, T. R. Brownstein M. J. Hodin, T. R. Casavant, T.L., Cabeat, T. R. Brownstein M. J. Hodin, T. R. Casavant, T.L., Cabeat, T. R. Brownstein M. J. Hodin, T. R. Casavant, T.L., Cabeat, T. R. Brownstein M. J. Hodin, T. R. Casavant, T.L., Cabeat, T. R. Toshivnki, S. Cabeat, M.	Db 1335 CAGTCTTCGGACTTGCTTGGAGATGTTCTTTGTGGTCCCTGCACTGATCACAGCTTCG 1394 Oy 1281 ATATCACAGAGATGCTGGTGCACCTGTCTATGAGTTTCGGCACCGGCCTCAGTG 1340

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Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                     CAACACATGCTCAAGGTGCATTACCCGAAAATTCGGAGTGTCAGAAGACTGCCTCTACCTG
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                           AACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGGTGGTTC
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Center code: BCM-HGSC
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/clone="MGC:91193 IMAGE:7262439"
/tissue_type="PCR rescued clones"
/clone_Tib="NIH_MGC_244"
/note="Vector: pPCR-Script Amp SK(+)"
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                                                                                                        GCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCACGGACGAGGAGAAGTTACTG
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CGAGAAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGAT 330	281 210 341 · 270	4; DB 6; Length 1962; es 1; Indels 150; Gaps 1; ccaegerregarreacreacecaageaa 150	Patent: EP 1293569-A 736 19-WAR-2003; Helix Research Institute (JP); Research Association for Biotechnology (JP) Location/Qualifiers 11962 11962 /organism="Homo sapiens" /mol_type="unassigned DNA" /dh_xref="taxon_9606"	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 sogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J.I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R., Yamamoto, J.I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and Masuho, Y. Masuho, Y. Full-length cDNAs	AX714052 Sequence 736 from Patent EP1293569. AX714052 AX714052.1 GI:2988980 Homo sapiens (human)	1651 CTGATCCTGCCTCCGACATGCTCCACAGTCCTCTTTCTTCCTTAACTTTCCTCT 1710	
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1351 ACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTTGTGTTCCGTTGGT 1410 1422	1231 GACTTGCTTGGAGATGTTGTTGTGGTCCCTGCACTGATCACAGCTCGATATCACAGA 1290	TCCCTTGCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAGTATTTGCACCTT TCCCTTGCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAGTATTTGCACCTT TCCCTTGCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAGTATTTGCACCTT TCCCTTGCCCTCCATCTGATACAAAACATCCTGCACATCCCGAAATCCGAGACAGTCTTCTG TTGGCTAATGAAATACTTCCATGACAAAGCACTCCCCTGACTGA	991 GATCTATTGTCTCAGAAAGCATTTAAAGCAATTCCTTCCATCATCGAGGAGTCAATAACCAC 1050	TCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAACCCTCCAAGGAGCTGCTGAGCCCTCAGCCTTGAGGCCCTGAGGACAAAACCCTCCAAGGAGCTGCTGAGCCCTCAGCCCTCAGGAGAAAACCCTCCAAGGAGCTGCTGACCCCTCAGCCTCTAAGGAGCCTCCAGGAGAAAACAAAAGTCTTTCGAGGGGTTGATGATGGTGCTTTCTTT	822 GAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTA 881 751 TTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTTGGAGGCCCATGAT 810		582 CCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCC 641 511 TATGAGGACGTGCTGGTTGTGGTCGTCCAGGTACCGGCTAGGAATATTTTGGTTTTCACC 570

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Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,B., Omura,Y., Abe,K.,
Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Yamamoro,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
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Direct Submitseion

Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: RAB and
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CCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCC
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/mol_type="mRNA"
/db_xref="teaxon:9606"
/clone="NT2RI2001010"
/cell_line="NT2"
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/clone_lib="NUTZRI2"
/clone_lib="NUTZRI2"
/note="cloning vector: pME188FL3-mRNA from NT2 neuronal
precursor cells treated 2-weeks mitotic inhibitor after
5-weeks retinoic acid (RA) induction.-majorly NT2 neuron"
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 GACCTGTCTCTGTGGCCAGCTTATAATCTGACTGAGCAGTACCTCCAGCTGGACTTGAAC
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Published Only in Database (2004)
2 (bases 1 to 1728)
Miyazaki,M., Yamashita,T., Taira,H. and SuDirect Submission
Submitted (04-AUG-2004) Masao Miyazaki, RIResearch, Supra-Biomolecular System Resear Wako-shi, Saitama 351-0198, Japan
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Canis familiaris cauxin mRNA for carboxylesterase-like urinary
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Fax:81-48-467-9620)
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931 CAGAAAACAAAGTCTTTCACTCGAGTGGTTGATGGTGCTTTCTTT	93 91
871 TCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAACCCTCCAAGGAGCTGCTGACCCTCAGC 930	87 85
811 TATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAATGCGTCAGAC 870 	81 79
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631 TGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGC 690	<u> </u>
GGGATCAG GGACCAG	
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CCAGGAGGTGCC	4. 4.
391 AACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTC 450	u u
331 CAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTG 390	W W
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ω σ	CTTCCTTAACTTTCCTCTCT 1710	TTTGGACCAGCACCATCCCC 1650	ACCTCCAGCTGGACTTGAAC 1590	CCGGGAATCCTAATGGGAAC 1530	ACGGAGGAGGAGTTACTG 1470 	FICCGCTTTGTGTTCGGTGGT 1410 	CGGCCTCAGTGCTTTGAAGAC 1350	GTCACAGCTCGATATCACAGA 1272

Search completed: June 14, 2005, 22:52:51 Job time: 7589.61 secs

Run

AGENCOURT BP444116 BP445396 BP447764 BP441209

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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 742)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                                                          Submitted (16-NOV-2003) Celera Genomics, Rockville, MD 20850, USA
This sequence was made by sequencing genthem based on alignment.

Location/Qualifiers
                                                                                                                                                                                 2 (bases 1 to 1680)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1680) Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous
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  /organism="Mus musculus"
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/db_xref="taxon:10090"
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/locus_tag="HCM5231"
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Pred. No. 3.8e-108;
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                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                    1 (bases 1 to 576)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Unpublished (1999)
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603033738F1 NIH_MGC_115 Homo
                                                                                           found through the I.M.A.G.E. Consortium/LLNL
http://image.llnl.gov
Plate: LLAM11435 row: 1 column: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
                                                                                                                                         CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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                                                               quality sequence start: 6 quality sequence stop: 565.
/organism="Homo sapiens"
/mol_type="mRNA"
                                1. .576
                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                             bp mRNA linear EST 04-OCT-2001 sapiens cDNA clone IMAGE:5174937 5',
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                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 160)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                           AY414459.1 GI:39770421
                                                                                                                                                                                                                                     genomic survey sequence
                                                                                                                                                                                                                                                     Homo sapiens CES2 gene,
                                                                                                                                                                                                                                                                       AY414459
                                Inferring nonneutral evolution from human-chimp-mouse orthologous
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nilarity 96.4%;
Conservative (
                                                                                                                                                                          sapiens (human)
   302 (5652), 1960-1963 (2003)
                                                                                                                                                                                                                                                       1680 bp
VIRTUAL
                                                                                                                                                                                                                                                        TRANSCRIPT,
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linear

GSS 17-DEC-2003

partial sequence,

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CCTATGAGGACGTGCTGGTTGTGGTCGTCCAGTACCGGCTAGGAATATTTGGT 561
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/clone lib=NIH MGC 115"
/note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: ECCRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69: Library is
oligo-dT primed and directionally cloned (EccRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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/clone="IMAGE:5174937"
/lab_host="DH10B"
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Pred. No. 3.8e-107;
0; Mismatches 14;
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Submitted (16-NOV-2003) Celera
Rockville, MD 20850, USA
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, N.D. and Cargill, M.
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               GTGGGGTGGCCATCATCCCTTACCTGGAGGCCCATGATTATGAGAAGAGTGAGGACCTGC
                                        TGTCTTCGCTTGTTGTGTCCCCCATATCCCCAAGGACTCTTCCACGGAGCCATCATGGAGA
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/mol type="genomic DNA"
/db xref="taxon:9606"
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/locus_tag="HCM5231"
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REFERENCE

HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus

AK033563 AK033563.1 GI:26329244

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

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                                        GACAGAGACTCAAAGAACCGCGGGTGGATTTTTGGACCAGCACCATCCCCC
                                                                                ACTGGCCGCTGTTCGACCAGGAGGAGCAATACCTGCAGCTGAACCTACAGCCTGCGGTGG
                                                                                                                      TGTGGCCAGCTTATAATCTGACTGAGCAGTACCTCCAGCTGGACTTGAACATGAGCCTCG
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                                                                                                                                                                                                         cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in I Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed prepare mouse tissues.
                                                                                                                                                                                                                                                                                                                  Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GS RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yok Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
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                                                                                                                                            prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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RESULT 6 AK077248 LOCUS DEFINITION Mus musculus 11 RIKEN full-lengt product:similar	Oy 1600 GGACAGAGACT	1543	Qy 1540 CTGTGGCCAGC	Db 1483 ATGATGAAGTA	1435	1420	Db 1375 CCCTATGTGAA	Qy 1360 GCTTTTGTCA	Db 1315 GCTCCTGTCTA	1200	240	98	ду 1180 салтасттсс	1138	Oy 1120 CTCCATCTGA	1078	Qy 1072 ATGAAGGAGGCTCCT-	Db 1018 TTTCACCCTG	958	952	Db 898 CTAAGAGGCA	Qy 892 CTGAGGACAA	Db 838 AGAATAGTGG	Оу 832 САССТССТТС	784	770	0y /12 GITTCTAGIC	664	
2687 bp mRNA linear HTC 03-APR-2004 11 days pregnant adult female ovary and uterus cDNA, nngth enriched library, clone:5031415B19 .ar to CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1)	GGACAGAGACTCAAAGAACCGCGGGTGGATTTTTGGACCAGCACCATCCCCCTGA 1654	TACTOSCCTOTGATGACCATGATGAGCAGTACCTGCAGCTGGACATCCAGCCTTCTGTG 1602	TTATAATCTGACTGAGCAGTACCTCCAGCTGGACTTGAACATGAGCCTC 1599	AIGAIGAAAIACIGGGCTACCTTTGCTCGAACCGGGAATCCTAATGGGAACGACCTGTCT 1539	TTCCTTACACTGAGGAAGAGGAGCAACTAAGCAGAAGG 1482	TTCGAAGGAGC	CCTATGTGAAGGCTGACCATGGTGATGAAATTTTCCTTGTCTTTGGCTACCAGTTCGGT 1434	14	GCTCCTGTCTATGAGTTTCCAACATCGACCCAGCTTCTTGAAGACACGAAGCCA 1359 GCTCCTGTCTACTTCTATGAGTTTCCAACATCGACCCAGCTTCTTCAAGGATTTTCAGGCCA 1374	TGTTCGTGATCCCTGCACTACAAGTAGCACATTTTCAACGTTCCCAT 1314	-	Д ,				CTCAGAAAATA		TITCACCCTGTCCCCAGCATCATTGTTATCAACAATGATGAGTTGGCTTCCTGCTCCT 1071	GGTGTGGTGGATGGAGAGTTCCTACCCAAGCATCCTCAGGAGCTGATGGCCTCTAAGGAT 1017	1011	CTAAGAGGCAAGAATGAAGCAGAGATGCTGGCTATTAATAAGGTCTTCAAAATCATCCCT 957		AGAATAGTGGCCAATCTATCTGGCTGTGCAGCTGTGAACTCAGAGACCCTGATGTGCTGC 897	ω .	AGTGGAGTAGCTGTGCTCCCTGATCTTATCTCCAGCTCCTCTGAGATGGTTCAC 837		GILITUTAGICTTATACTGTCTCCCATGGCCAAAGGCTTATTCCACAAAGCCATCATGGAG 771	CACTTTGGAGGCAACCCTGACCGAGTCACCATTTTTGGAGAGTCAGCGGGTGGCACAAGT 723	

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                                                                                                                                    Direct Submission
Submitted (16-ARR-2002) Yoshihide Hayashizaki, The Institute of Submitted (16-ARR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoham RIKEN Yokohama 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                        Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P. Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Horti, F., Imotani, K., Ishii, Y., Ich, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (Dases I to 2687)
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FANTOM Consortium.
Functional annotation of a full-length
Nature 409, 685-690 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria;
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Please visit our web site for further details.
URL:http://fantom.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                                                                                            TACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCAC
                                                                                                                                                                                                                                            TTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTA---GATCAACATGCTCAAGGTGCAT
                                                                                                                                                                                                                                                                                     GCACCTCCTGAGGCCCCTGAGCCATGGAGTGGGGTGAGGGATGGGACCTCACATCCAAAC
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GGCATGGCTTCCATGTATGATGGATCCATGCTGGCAGCAACTGAGGATGTGGTGGTGGTC
                             GGCTCAGCCTCCATCTTGATGGGTCCGCCCTGGCTGCCTATGAGGACGTGCTGGTTGTG
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PDRVTIFGESAGGTSVSSHVVSPMSQGLFHGAIMESGVAVLPDLISSSEMVHRIVAN
LSGCAAVNSETLMCCLGKKNRAEMLAINKVFKIIFGVDGFFLFKHPQELMASKDFHP
VPSIIGINNDEYGMILPTIMDDAQKIEBITTRKTLPAVLKGTALKMMPLPFECGDLMEE
YMGDTEDPETLQAQFREMKGDFMFVIPALQVAHFQRSHAPVFYEFQHRPSFFKDFRP
PYVKADHGBEIFLVFGYQFGNIKLPYTEBEEQLSRINKYWANFARHGNPNSEGLFYW
PPYVKADHGBEIFLVFGYQFGNIKLPYTEBEEQLSRINKYWANFARHGNPNSEGLFYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="unnamed protein product; putative similar to CARBOXYLESTERASE PRECURSOR (EC 3.1.1.) (ALI-ESTERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAINE ESTERASE) (METHYLBUTYRASE) [MESOCTICETUS BUTTANDE (SPIR 035533, evidence: FASTY, 03$1D, 100$length, match=1677)"
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/tissue_type="ovary and uterus"
/clone_lib="RIKEN full-length enriched mouse
/dev_stage="11 days pregnant adult"
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/db_xref="FANTOM_D
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b_xref="taxon:10090"
lone="5031415B19"
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Pred. No. 1.2e-101;
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E Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Myyazaki, A., Murata, M., Koya, S., Kurihara, C., Matsuyama, T., Myzazaki, R., Ohno, M., Ohsato, N., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Takaka, A., Takaka, T., Tomaru, A., Takahashi, F., Takaku-Akahira, S., Muramateu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                           Group Phase I & II Team.
Analysis of the mouse transcriptome based of 60,770 full-length cDNAs
    Submitted (16-JUL-2001) Yoshihide
                                                                                                                                                                                                                                                                                                                                                                                                  The FANTOM Consortium and the RIKEN Genome Exploration Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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MUS MUSCULUB 0 day neonate thymus CDNA, RIKEN full-length enriched library, clone:A430088E12 product:similar to CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ALI-ESTERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAINE ESTERASE) (PROCAINE ESTERASE) (METHYLBUTYRASE) (MEGOCTICETUS auratus), full insert sequence.
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Please visit our web site for further details.
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CAGCCACTGAGGATGTGGTGGTGGTTACTCAGTACCGCCTGGGAATCCCGGGCTTTT
                                  CTGCCTATGAGGACGTGCTGGTTGTGGTCCTCCAGTACCGGCTAGGAATATTTGGTTTCT
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(ALI-ESTERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAINE
ESTERASE) (PROCAINE ESTERASE) (METHYLBUTYRASE)
[Mesocricetus auratus] (SPTR (035533, evidence: FASTY,
70.7%ID, 99.2%length, match=1672)"
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/dev_stage="0 day neonate"
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

So (bases I to 1958)

Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Pukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hiranoto, K., Hiraoka, T., Hirozane, T., Hayashida, K., Hayatsu, N., Hiranoto, K., Konno, H., Kouda, M., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M. and Hayashizaki, Y. Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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1958 bp mRNA linear HTC 03-APR-2004 Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130231C15 product:similar to LIVER CARBOXIESTERASE PRECURSOR (EC 3.1.1.1) [Mesocricetus auratus], full insert
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URL:http://fantom.gsc.riken.jp/.
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Please visit our web site for further details.
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Division of Experimental Animal Research in Riken contributed to
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similar to LIVER CARBOXYLESTERASE PRECURSOR (EC 3.1.
[Mesocricetus auratus] (SWISSPROT|Q64419, evidence:
78.4%1D, 100%length, match=1674)"
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/clone_Tib="RIKEN full-length
/dev_stage="adult"
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/db_xref="taxon:10090"
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/strain="C57BL/6J"
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Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Please visit our web site for further details.
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Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute Physical Research (RIKEN), Laboratory for Genome Physical Research (18-APR-2002) Yoshihide Hayashizaki, The Institute Physical Research (18-APR-2002) Yoshihide Hayashizaki, The Institute Physical Research (18-APR-2002) Yoshihide Hayashizaki, The Institute Physical Research (18-APR-2002) Yoshihide Hayashizaki, The Institute Physical Research (18-APR-2002) Yoshihide Hayashizaki, The Institute Physical Research (18-APR-2002) Yoshihide Hayashizaki, The Institute Physical Research (18-APR-2002) Yoshihide Hayashizaki, The Institute Physical Research (18-APR-2002) Yoshihide Hayashizaki, The Institute Physical Research (18-APR-2002) Yoshihide Hayashizaki, The Institute Physical Research (18-APR-2002) Yoshihide Hayashizaki, The Institute Physical Research (18-APR-2002) Yoshihide Hayashizaki, The Institute Physical Research (18-APR-2002) Yoshihide Hayashizaki, The Institute Physical Research (18-APR-2002) Yoshihide Hayashizaki, The Institute Physical Research (18-APR-2002) Yoshihide Hayashizaki, The Institute Physical Research (18-APR-2002) Yoshihide Hayashizaki, The Institute Physical Research (18-APR-2002) Yoshihide Hayashizaki, The Institute Physical Research (18-APR-2002) Yoshihide Hayashizaki (18-APR-2002) Yoshihide Hayashizaki (18-APR-2002) Yoshihide Hayashizaki (18-APR-2002) Yos
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Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
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Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
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URL:http://fantom.gsc.riken.jp/.
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       GTGCCTCCAGAACTC-----AGAGTGGCTGCTCTAGATCAACACATGCTCAAGGTGCA
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ENVVVVTIQYRLGIWGFFSTGDEHSRGNWGHLDQVAALXTTDVKFIAGLVATLSGCKTT
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TSAVMYHCLRQKTEDELLETSLKLNLFKLDLLGNFKRSYPFLVIOGVVLPKAPEEI
LAEKSFSTVPYIGGINKQEFGWIIFTLMGYPLAEGKLDQKTANSLLMKSYPTLKISEN
MIPVVARKYLGGTDDLTKKXDLFQDIAADVVFGVPSVLVSRSHRDAGASTYMYEFEYR
PSFVSAMRPKAVIGDHGDEIFSVFGSPFLKOGASEESTNLSKWVMKFWANFARNGNPN
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/mol_type="mRNA"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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GTTTGAGTATCGCCCAAGCTTTGTATCGGCCATGAGACCCAAGGCAGTAATAGGAGACCA
                                                                                                      CCCTGCACTGATCACAGCTCGATATCACAGAGATGCTGGTGGACCTGTCTACTTCTATGA 1319
                                                                                                                                                                                     CCTGCACATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAGCA 1199
                                                                                                                                                                                                                                                                                                                CGCTGAAGGCAAACTGGACCAGAAGACAGCCAATTCTCTCTTGTGGAAGTCCTACCCAAC 1220
                                                                                                                                                                                                                                                                                                                                                                                          AGTGGGCATCAACAAGCAAGAGTTTGGCTGGATCATTCCAACGCTTATGGGCTATCCACT 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTTCGGCACCGGCCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCA 1379
                                                                            ACTTAAAATCTCTGAGAATATGATTCCAGTGGTCGCTGAGAAGTATTTAGGAGGGACAGA
                                                                                                                                                                                                                                                                                                                                                       TCCTGAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAAC---AT 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                 CATCGGAGTCAATAACCACGAGTGTGGCTTCCTGCCTGTGTGAAGGAGG-----C 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTGCCAAAGGCACCAGAAGAGATCCTGGCTGAGAAGAGTTTCAGCACTGTCCCCTACAT 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGACCCTCAGCCAGAAAACAAAG-----TCTTTCACTCGAGTGGTTGATGGTGCTTT 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGAAGACAGAGGATGAACTACTGGAGACCTCACTAAAATTGAATCTTTTTAAACTGGA
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translation="MTAQSRSPTTPTFPGPSQRTPLTPCPVQTPRLGKALIHCWTDPG

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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@kfz-heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZ)644N9935) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomeforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp434N0935 further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 2888)

Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
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AL713761
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                                                                                                                                   /gene="DKFZp434N0935"
954. .2777
                                                                                                                                                                                                              /tissue type="restis"
/clone_Tib="434 (symonym: htes3). Vector pSport1; host
DH10B; sites NotI + SalI"
/dev_stage="adult"
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/protein id="CAD28531.1"
/db_xref="CI:19584507"
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/codon_start=1
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/mol_type="mRNA"
/db_xref="rzPp:DKFZp434N0935"
/db_xref="taxon:9606"
                                                                                                                                                                                              note="carboxylesterase 2
                                                                                                                                                                                                                                                                                                               clone="DKFZp434N0935"
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QPLGEQQRVRRQRTETSEPTMRLHRLRARLSAVACGLLLLLVRGQGQDSASPIRTHT
GQVLGSLVHVKGANAGYQTELGIPFAKEPLGFLRFAB PEDEPESWSGVBDGTTHPAMCL
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STVANILSACDQVDSEALVGCLEGKSKESILAINKFPKHIFGVALLPGLIALPFTGE
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LKNIRPPHMKADHVKTTEEESQLSRKMMKYWANFARKGNPNGCSLFHWPLFDQEEQYL QLNLQPAVGRALKAHRLQFWKKALPQKIQELEEPEERHTEL"

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ORIGIN Matches 850; Query Match Best Local Similarity 1846 1786 1666 1606 1546 1486 1426 1306 1246 2020 1960 1906 1726 1366 893 833 773 713 653 593 533 473 413 353 296 236 176 116 GCCATGAAGGCTCTAACCTGCCGGTGATGGTGTGGATCCACGGTGGTGCGCTTGTTTTTG CCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGTGTCCCAGGAGGTGCCTTCAAGACTG ACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCACG GGGTCCAAACCTTCCTGGGAATTCCATTTGCCAAGCCACCTCTAGGTCCGCTGCGATTTG CTGTGAACGTGTTCCTCGGAGTCCCCTTTGCTGCTCCCCCGCTGGGATCCCTGCGATTTA 235 AGGTGGTTGCACATTTCTGTGGTAACAATGCGTCAGACTCTGAGGCCCCTGCTGAGGTGCC TCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGCGAGTCCGCGGGAGCCATAAGTG GGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCCTGGGTCCAGAAGAACATCGAGT 652 TCGTCCAGTACCGGCTAGGAATATTTGGTTTCCTTCACCACATGGGATCAGCATGCTCCGG GCATGGCTTCCTTGTATGATGGTTCCATGCTGGCTGCCTTGGAGAACGTGGTGGTCGTCA 1665 TCCCTTCCGACTCCATGTCTGAGGACTGCCTGTACCTCAGCATCTACACGCCGGCCCATA 1545 CACCCCTGAGCCCCTGAATCTTGGAGTGTGTGAGGGATGGAACCACCCATCCGGCCA 1425 GGAACACCAGGCTGGGATGGATTCAGGGCAAGCAAGTCACTGTGCTGCGGAAGCCCTGTGC 175 TGCGGGGCAAGAGTAAAGAGGAGATTCTTGCAATTAACAAGCCTTTCAAGATGATCCCCCG CGGTGGTGGCCAACCTGTCTGCCTGTGACCAAGTTGACTCTGAGGCCCCTGGTGGGCTGCC GTGGGGTGGCCATCATCCCTTACCTGGAGGCCCATGATTATGAGAAGAGTGAGGACCTGC TGTCTTCGCTTGTTGTGTCCCCCATATCCCAAGGACTCTTCCACGGAGCCATCATGGAGA ACTTTGGAGGCAACCCTGACCGTGTCACCATTTTTGGCGAGTCTGCGGGTGGCACGAGTG GCAACTGGGGCTACCTGGACCAAGTGGCTGCACTACGCTGGGTCCAGCAGAATATCGCCC TCATCCAGTACCGCCTGGGTGTCCTGGGCTTCTTCAGCACTGGAGACAAGCACGCAACCG GCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCCTATGAGGACGTGCTGGTTGTGG TGTGTCTACAGGACCTCACCGCAGTGGAGTCAGAGTTTCTTAGCCAGTTCAACATGACCT TGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGA---TCAACACATGCTCAAGGTGCATT CGAACCCGCAGCCTGCATCGCCCTGGGATAACTTGCGAGAAGCCACCTCCTACCCTAATT ĠĠĀĊĊĀĊĀĊĀCĀCĀGĠĠGCĀĠĠŤĠĊŢĠĠĠĠĀĠŢĊŢŢĠŤĊCĀŤĠŤĠĀĀĠĠĠĊĠĊĊĀĀŤĠĊCG 1305 TGAGGACAAAACCCTCCAAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACTC TTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTATTCCACAAAGCCATCATGGAGA Conservative 19.8%; .. Score 345.8; DB 3; Pred. No. 3.6e-87; Mismatches 617; Indels 84; Length 2888; Gaps 592 532 472 412 295 2079 832 1905 772 1845 1485 352 1365 952 2019 892 712 1785 1725 1605 5

7 GCCGGGCTCTGAAGGCCCACAGGCTCCAGTTCTGGAAGAAGGCGCTGCCCC 2727	pb 2677
1 GACAGAGACTCAAAGAACCGGGGTGGATTTTTGGACCAGCACCATCCCCC 1651	Оу 1601
7 ACTGGCCGCTGTTCGACCAGGAGGAGGAATACCTGCAGCTGAACCTACAGCCTGCGGTGG	Db 2617
	Qy 1541
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	Qy 1481
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	Qy 1421
7 CGCACATGAAGGCAGACCATGTTAA	Db 2497
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	Db 2437
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	Qy 1241
O AGTACATTGGGGACAATGGGGGATCCCCAGACCCTCCAAGGCGCAGTTCCAGGAGATGATGG	Db 2320
	Оу 1181
o TGCAGAAAATGTTAACGCTGCTGATGTTGCCTCCTACATTTTGGTGACCTGCTGAGGGAGG	Db 2260
1 TCCATCTGATACAAAACATCCTGCACATCCCGCCTCAGTATTTGCACCTTGTGGCTAATG 1180	Оу 1121
O AGGTCATGAGGATCTATGATACCCAGAAGGAAATGGACAGAGAGGGCCTCCCAGGCTGCTC 2259	Db 2200
1TATGAAGGAGGCTCCTGAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCC 1120	Оу 1071
0 TTCAGCCTGTCCCTAGCATTGTTGGTGTCAACAACAATGAATTCGGCTGGCT	Db 2140
3 TTAAAGCAATTCCTTCCATCATCGGAGTCAATAACCACGAGTGTGGCTTCCTGCTGCC 1070	Оу 1013
O GAGTGGTGGATGGGTTTCCTGCCCAGGCACCCCCAGGAGCTGCTGGCCTGCCGACT 2139	Db 2080

RESULT 11
HSM806270
LOCUS
DEFINITION
ACCESSION SOURCE ORGANISM VERSION KEYWORDS REFERENCE COMMENT CONSRTM TITLE JOURNAL AUTHORS Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd
Braunschweig/Germany) within the cDNA sequencing consortium of th Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Weil, B., Amid, Obanger, A., Fobo, G., Han, M. and Wiemann, S.

The German cDNA Consortium
Direct Submission
Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Homo sapiens mRNA; cDNA BX538086 Homo sapiens HTC BX538086.1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalia; Eutheria; Primates; Catarrhini; Hominidae; German Genome Project Homo sapiens (human) HSM806270 (bases 1 to 3909) GI:31874222 3909 bp mRNA 1 DKFZp686H0466 (from linear HTC 22-SEP-20 clone DKFZp686H0466). Weil, B., Amid, C. Euteleostomi; HTC 22-SEP-2004

B

GAGTGGTTGATGGTGCTTTCCTTACCTAATGAGCCTCTAGATCTATTGTCTCAGAAAGCAT 1012

This clone (DKFZp686H0466) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany

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http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686H0466
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
TCATCCAGTACCGCCTGGGTGTCCTGGGCTTCTTCAGCACTGGAGACAAGCACGCAACCG
                          TCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACCACATGGGATCAGCATGCTCCGG
                                                                                                                                                                                GCCATGAAGGCTCTAACCTGCCGGTGATGGTGTGGATCCACGGTGGTGCGCTTGTTTTTG
                                                                                                                                                                                                             CCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGTTCCCAGGAGGTGCCTTCAAGACTG
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91 GGGCCTTCTGCTGAAGGGCCACAGAGGAACACCAGGCTGGGATGATCAGGGCAAGCAA	ttch al Similari	High qual	ct: Shultz MA of Molecular Biosciences, School of Veter irsity of California, Davis Haring Hall, One Shields Avenue, Davis, CA 530 752 0793 530 752 4698 : mashultz@ucdavis.edu ige phred score is 20 or better. All poor q	Shu Shu Padu Plop Gene Sequ	
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Contact: MGC help deek
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (DNA Sequencing by: Baylor College of Medicine Human
                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLNI at: http://image.llnl Series: IRAK Plate: 42 Row: p Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
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Direct Submission
Submitted (19-DEC-2001) National Institutes of Health, Mammalian
Submitted (19-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                               passed the following identity to protein
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Guntaratne, P.H., Garcia, A.M., Lu, X., Huly.
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart
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Mus musculus, clone IMAGE:5123923,
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/clone="IMAGE:5123923"
/tissue_type="Liver, normal.
/clone_Tib="NCI_CGAP_Li9"
/lab_host="DH10B"
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                                                                                                                                              Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1826)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                    Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CR618303 1826 bp full-length cDNA clone CS0DE014YC12
                                                                                                                                    division of Invitrogen
                                                                                                                                                                                                                                                                                                         Paraday Avenue
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       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODE014YC12"
/tissue_type="Placenta"
/plasmid="pCMVSPORT_6"
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                                           CACGAGTGTGCTTCCTGCTGCCTATGA 1075
                                                                                                                                    AAGCTGAAAAATACTATCTATCCTCTCACCGTTGATGGCACTGTCTTCCCCAAAAAGCCCC
                                                                                                                                                       GATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAATGCGTCA
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Pred. No. 1.2e-73;
0; Mismatches 421;
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More information available at
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Location/Qualifiers
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TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: EAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-122001
CURRENT APPLICATION NUMBER: US/10/023,515
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/256,369
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/279,508
PRIOR FILING DATE: 2000-12-18
INUMBER OF SEQ ID NOS: 6
SOFTWARE: FEATURE 2001-03-28
INUMBER OF SEQ ID NOS: 6
SOFTWARE: FEATURE:
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Patent No. 6664091
GENERAL INFORMATION:
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Score 508.6; DB 4; Pred. No. 3.2e-150;

Length 965;

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APPLICANT: Wang, Dunrui
APPLICANT: Yang, Yonghong
APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Reena
APPLICANT: Drmanac, Radoje T.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6783969el Nucleic Ac:
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 155
ILENGTH: 965
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (128)...(925)
US-09-799-451-155
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APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Zhang, Jie
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Mang, Vunqing
APPLICANT: Mangazaki, Victor
APPLICANT: Chen, Rui-hong
APPLICANT: Wang, Diniwei
APPLICANT: Wang, Duriui
APPLICANT: Wang, Duriui
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Tom
APPLICANT: Wehrman, Tom
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Xue, Aidong J.
Zhao, Qing A.
Wang, Jian-Rui
Ma, Yunqing
Yamazaki, Victoria
Chen, Rui-hong
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Sequence 3799, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GEI
TITLE OF INVENTION: WITH HUMAN DISEASE, METH,
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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US-09-949-016-3799
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Pred. No. 1.2e-117;
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RESULT 5
US-09-949-016-555
Sequence 555, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
Craig et al.
                                                                                                    PILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
VNUMBER OF SEQ ID NOS: 207012
SOPTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 555
                                    US-09-949-016-555
 Query Match
                                                   LENGTH: 2169
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                              APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
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APPLICANT: Danks, Mary K.
APPLICANT: Danks, Mary K.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of TITLE OF INVENTION: Tumor Cells
FILE REFERENCE: SJ-0005
CURRENT APPLICATION NUMBER: US/09/595,682B
CURRENT FILING DATE: 2000-01-16
FRIOR APPLICATION NUMBER: 60/075,258
PRIOR FILING DATE: 1998-02-19
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Datentin Ver. 2.0
SEQ ID NO 27
LENGTH: 2191
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                    Query Match
Best Local Similarity
Matches 876; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27, Application US/09595682B Patent No. 6800483 GENERAL INFORMATION:
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          CGAACCCGCAGCCTGCATCGCCCTGGGATAACTTGCGAGAAGCCACCTCCTACCCTAATT
                                     GGGTCCAAACCTTCCTGGGAATTCCATTTGCCAAGCCACCTCTAGGTCCGCTGCGATTTG
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ilarity 56.5%;
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Pred. No. 1.2e-117;
0; Mismatches 639;
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APPLICANT: Danks, Mary K.
APPLICANT: Potter, Philip M.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: Tumor Cells
FILE REFERENCE: SJ-0005
FURRENT APPLICATION NUMBER: US/09/595,682B
CURRENT FILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: 60/075,258
PRIOR FILING DATE: 1998-02-19
PRIOR APPLICATION NUMBER: PT/US99/03171
PRIOR APPLICATION NUMBER: PT/US99/03171
PRIOR PILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 1171
TYPE: DNA
ORGANISM: Oryctolagus cuniculus
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match 20.8%;
Best Local Similarity 54.8%;
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Pred. No. 8.8e-104;
0; Mismatches 649;
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Sequence 3, Application US/09264737A

Patent No. 6107549

GENERAL INFORMATION:
APPLICANT: Feng, Paul C.C.
APPLICANT: Reng, Paul C.C.
APPLICANT: Ruff, Thomas G.
TITLE OF INVENTION: Engineering Plant Resistance to Pyridines via
TITLE OF INVENTION: Expression of Esterase Enzymes
FILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance
CURRENT APPLICATION NUMBER: US/09/264,737A
CURRENT FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: 60/077,377
EARLIER APPLICATION NUMBER: 60/077,377
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 1701
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; ORGANISM: Rabbit
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Best Local Similarity 54.8%;
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Pred. No. 5.2e-102;
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                                                                                                CCTTTGCTCGAACCGGGAATCCTAATGGGAACCACCTGTCTCTGTGGCCAGCTTATAATC 1558
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                        TGACTGAGCAGTACCTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAAC 1618
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CURRENT APPLICATION NUMBER: US/09/810,861B
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/190,440
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: human acetylcholinesterase gene optimized for OTHER INFORMATION: expression in plants
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706 ATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTATTCCACAAAGCCATC
                                                                                                                                                                                                                                                                                      GCCTCCTTGGACGTGTACGATGGCCGCTTCTTGGTACAGGCCGAGAGGACTGTGCTG
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                                                                                                                                                    GCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCCTGGGTCCAGAAGAAC
                                                                                                                                                                                                         GTGTCCATGAACTACCGGGTGGGAGCCTTTGGCTTCCTGGCCCTGCCGGGGAGCCGAGAG
                                                                                                                                                                                                                                           GTGGTCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACC---ACATGGGATCAGCAT 585
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Arntzen, Charles J.
Mason, Hugh S.
                                        GTGGCAGCCTTCGGGGGTGACCCGACATCAGTGACGCTGTTTGGGGAGAGCGCGGGAGCC
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                                                                            ATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGCGAGTCCGCGGGAGCC
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Pred. No. 4.8e-33;
D; Mismatches 266; Indels 12;
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US-07-732-962A-1
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                     Query Match
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/732,962A
FILING DATE: 19910722
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION UNMER: 28,678
REFERENCE/DOCKET NUMBER: 3930
TELECOMMUNICATION INFORMATION:
TELEPIONE: (212) 977-9550
TELEFAX: (212) 664-0525
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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TOPOLOGY: linear
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STATE: New York
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Local Similarity 55.1%;
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                                   CCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCACGCC
                                                                                                                                          CTGCCACCGGAGCCCAAGCAGCCTTGGTCAGGGGTGGTAGACGCTACAACCTTCCAGAGT
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 CCCAACCGTGAGCTGAGCGACGGCCTGTACCTCAACGTGTGGACACCATACCCCCGG
                                                                      GTCTGCTACCAATATGTGGACACCCTATACCCAGGTTTTGAGGGCACCGAGATGTGGAAC
                                                                                                     TTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGATCAACACATGCTCAAGGTGCATTAC
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EXPRESSION OF ENZYMATICALLY ACTIVE
RECOMBINANT HUMAN ACETYLCHOLINESTERASE
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                                                                                                                                                                                                                                                                                  Mismatches
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ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REPERENCE/DOCKET NUMBER: 39304-B-PCT/JPW/EAB

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEFAX: (212) 664-0525

TELEFAX: (212) 664-0525

TELEFAX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 1845 base pairs
; NAME/KEY:
; LOCATION:
PCT-US92-06106-1
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PCT-US92-06106-1
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GENERAL INFORMATION:
APPLICANT: Fischer, Meir
TITLE OF INVENTION: ENZYMATICALLY
TITLE OF INVENTION: ACETYLCHOLINES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/0610
FILING DATE: 19920722
                                                  MOLECULE TYPE:
FEATURE:
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MEDIUM TYPE: Floppy disk
                                                                                     TYPE: NUCLEIC ACID STRANDEDNESS: sing TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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              1..1842
                                   CDS
                                                                  DNA (genomic)
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Sequence 1192, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILLE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
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US-09-949-016-1192
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                                                                                         SEQ ID NO 1192
LENGTH: 2158
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                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Versio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                        TYPE: DNA
ORGANISM: Human
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Similarity 55.1%;
41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGGAGAGTGGGGTGGCCA 784
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                                                                                                                                                          Version
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                                                                                                                                                          4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   266;
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OF DETECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DETECTION
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION A

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-09-08

PRIOR PILING DATE: 2000-09-08

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-09-08

PRIOR PILING DATE: 2000-0
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US-09-949-016-1193
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Best Local Similarity 55.7
Matches 341; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1193, Application US/09949016 Patent No. 6812339
                                                                                                           SEQ ID NO 1193
   TYPE: DNA
ORGANISM: Human
                                                                       LENGTH: 2158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         646
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Patent No. 5891725
GENERAL INFORMATION:
GENERAL Soreq,
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APPLICANT: Zakut, Haim
APPLICANT: Zakut, Haim
APPLICANT: Eckstein, Fritz
TITLE OF INVENTION: Synthetic Antisense
TITLE OF INVENTION: Oligodeoxynucleotides
TITLE OF INVENTION: Containing Them
NUMBER OF SEQUENCES: 9
CORRESSPONDENCE ADDRESS:
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                        STATE: M
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STATE: Michigan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5, Application US/08318826A
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nilarity 55.1%;
Conservative
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                                                                                                                                                                                                                                                    Suite
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OTHER INFORMATION:
OTHER INFORMATION:
US-08-318-826A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
TENGTH: 2256 base pairs
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE:
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOKGT NUMBER: 2391.00001
FELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: doub
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                                                                                                                                                                GCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCCTGGGTCCAGAAGAAC
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GCCTCGGTGGGCATGCACCTGCTGTCCCCGCCCAGCCGGGGCCTGTTCCACAGGGCCGTG
                                                                                                     ATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGCGAGTCCGCGGGAGCC 705
                                                                                                                                                                                                                                      GTGGTCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACC---ACATGGGATCAGCAT 585
                                                                                                                                                                                                                                                                                GCCTCCTCCTTGGACGTGTACGATGGCCGCTTCTTGGTACAGGCCGAGAGGACTGTGCTG 690
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                               ATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTATTCCACAAAGCCATC 765
                                                                    GTGGCAGCCTTCGGGGGTGACCCCGACATCAGTGACGCTGTTTGGGGAGAGCGCGGGAGCCC
                                                                                                                                        GCCCCGGGCAATGTGGGTCTCCTGGATCAGAGGCTGGCCCTGCAGTGGGTGCAGGAGAAC
                                                                                                                                                                                                              GTGTCCATGAACTACCGGGTGGGAGCCTTTGGCTTCCTGGCCCTGCCGGGAGCCGAGAG
                                                                                                                                                                                                                                                                                                                 TCAGCCTC----CATCTTTGATGGGTCCGCCCTGGCTGCCTATGAGGACGTGCTGGTT 528
                                                                                                                                                                                                                                                                                                                                                                                                                        CCCAACCGTGAGCTGAGCGACTGCCTGTACCTCAACGTGTGGACACCATACCCCCGG
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ilarity 55.1%;
Conservative
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3, 4 and 6"
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Pred. No. 5.8e-33;
0; Mismatches 266;
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US-08-370-156-1
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Best Local 9
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GENERAL INFORMATION:
APPLICANT: Soreq,
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TELEPAX: (810) 689-4071
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: KOHN, Kenneth I.
REGISTRATION UNMBER: 9.955
REFERENCE/DOCKET NUMBER: P-30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: TRANSGENIC ANIMAL A TITLE OF INVENTION: ANTICHOLINESTERASE NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2256 base pai
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 55.1 nes 341; Conservative
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
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475 TCAGCCTC-----CATCTTTGATGGGTCCGCCCTGGCTGCCTATGAGGACGTGCTGGTT 528
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                                                                                                                                                                                                                                                                                                                                                      175 CCTGTGAACGTGTTCCTCGGAGTCCCCTTTGCTGCTCCCCCGCGCTGGGATCCCTGCGATTT
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E: Michigan
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                                                                                   GATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTCCCAGGAGGTGCCTTCAAGACTGGC
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                                                                                                                                                    CCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCACGCC 414
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P.O. Box 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zakut, Haim
Shani, Moshe
VENTION: TRANSGENIC ANIMAL ASSAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Soreq,
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Pred. No. 5.8e-33;
0; Mismatches 266;
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Search completed: June 14, 2005, 23:03:36 Job time : 296.702 secs



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Result
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Copyright (c) 1993 - 2005 Compugen Ltd
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          Abn84302 Human car
Adg89093 Human uro
Abg86169 Novel hum
Aad40574 Human dru
Acn42766 Human dia
Adb2205 Human cDN
Abx72267 Human NOV
Abg86170 Novel hum
Adr19681 Human cod
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Adf80130 Human car
Ada523013 Human car
Ada523013 Human car
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23-SEP-2002 (first entry)

ABN84302;

ABN84302 standard; cDNA; 2158

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Ada76491	Ada76547	Ada46060	Aca67707	Aca04294	Aca68601	Acd42065	Aca06084	Abx89411	Aca03873	Acd28810	Ab195693	Ab188204	Abk33640	Aae21514	Aaa96341	Aad08405	Aad00680	Abz24055	Aaf21884	Abn97359	Ab163768	Ab162492	Ab162491	ADZZ4051
Human PRC	Novel hum	Novel hum	cDNA enco	Human cDN	Novel hum	Human sec	cDNA enco	DNA encod	cDNA enco	Human sec	Human ang	Human PRO	cDNA enco	Human cDN	cDNA enco	Human sec	Human Hyd	CES2 rela	Human bre	Gene #385	Breast ca	Colon ade		н

ALIGNMENTS

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53010 nucleic acids, useful for diagnosing and treating e.g. vascular diseases, autoimmune diseases, or neurodegenerative diseases, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carboxylesterase; enzyme; human; analgesic; nootropic; antiinflammatory; diagnosis; gene therapy; gene; ss.
                                                                                                                  WPI; 2002-547936/58.
P-PSDB; ABB79537.
                                                                                                                                                                                                                         Curtis RAJ, Silos-Santiago I;
                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2000; 2000US-0256369P.
28-MAR-2001; 2001US-0279508P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-DEC-2001; 2001WO-US049075.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200250256-A2
                                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/product= "53010"
/note= "the CDS is also claimed in Claim 1"
/note= "the CDS is also claimed in Claim 1"
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174. .1838
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875 780 815

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The present nucleotide sequence, the coding region of which is also CC claimed, is that of cDNA encoding human 53010, a novel member of the CC carboxylesterase family. The invention provides 53010 nucleic acids, CC antisense molecules, expression vectors, host cells, transgenic animals, CC 33010 proteins, fusion proteins, antigenic peptides, anti-53010 CC antibodies and methods for detecting the presence of 53010 polypeptides or nucleic acids and polypeptides can act as novel diagnostic and CC polypeptide, and of modulating the activity of the polypeptide. The 53010 CC nucleic acids and polypeptides can act as novel diagnostic and CC therapeutic agents for controlling disorders involving aberrant or CC deficient hydrolysis of carboxylic esters. As 53010 mRNA is highly CC expression is regulated in some rodent pain models, 53010 molecules can also act as novel diagnostic targets and therapeutic agents for controlling neurological disorders, such as pain-related disorders. A CC claimed method of treating or preventing a disorder (especially a pain-created disorder) characterised by aberrant activity of a 53010 cc activity or expression. 53010 nucleic acids are also useful in chromosome CC expressing cell involves administering a compound that modulates 53010 cc arrays, for detection of variations or mutations, as surrogate markers and in bharmacocennomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 1746; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2158 BP; 515 A; 559 C; 509 G; 575 T; 0 U; 0 Other;
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                        TCCATCTTTGATGGGTCCGCCCTGGCTATGAGGACGTGCTGGTTGTGGTCGAG
                                                                                                                                                                            GGCTCCAAGCTCCCCGTCTTGGTGT
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04-FEB-2003;
27-MAR-2003;
08-MAY-2003;
19-MAY-2003;
The present invention describes the use of polypeptides related to urological disorders for identifying a compound capable of treating a unrological disorder, identifying a subject having a urological disorder, or treating a subject having a urological disorder. Also described: (1) a method for identifying a compound capable of treating a urological disorder; (2) a method for identifying a subject having a urological disorder; and (3) a method for treating a subject having a urological disorder. The compound has uropathic and cytostatic activities. The polypeptides related to urological disorder are useful for identifying a compound capable of treating a urological disorder, identifying a subject having a urological disorder. Disorders include urinary incontinence and benign prostatic hyperplasia. The present sequence encodes a human urological disorder related protein, which is used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                        Use of polypeptides related to urological disorders, e.g. 44390, 54181, 211 or for identifying a compound capable of treating a urological disorder or identifying and treating a subject having a urological
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18-JUL-2003;
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                                                                                                                                                                                                                                                                                                   Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-OCT-2004 (first entry)
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Query Match Best Local Similarity Matches 1654; Conserv

Conservative

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Gaps

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Score 1652.8; Pred. No. 0; 0; Mismatches

Sequence 1728

BP;

367 A; 483 C; 94.7%;

437 G; 441

T; 0 U; 멂 2; 6.

0 Other;

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The invention relates to an isolated polypeptide with signal sequences CC which allow it to be secreted extracellularly or membrane associated. The CC activity of polypeptides of the invention may be described as, CC extostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic, CC neuroprotective, immunosuppressive, haemostatic, antiinflammatory, CC cardiant, antiulcer, virucide, antithyroid, cerebroprotective, anorectic, CC useful in the treatment, or as a vaccine in the prevention of, cancer, CC wound healing disorders, infection, attherosclerosis, Parkinson's disease (CC useful in the prevention, activation, attherosclerosis, Parkinson's disease (CC uniflammation, neoplastic diseases, nervous system related disorder, CC inflammation, neoplastic diseases, nervous system related disorder, CC disorder disorder, pancreatitis, respiratory disorder, thyroid CC cardiovascular disorders, pancreatitis, respiratory disorder, thyroid developmental abnormality, gastrointestinal ulceration, neuropathy, CC haematological diseases, metabolic diseases, hyper-immunity, CC disorders e.g. hypothyroidism, brain damages, colitis, cone photo-CC transduction deficiency, neurological diseases, stroke, angiogenesis, covulation disorders, diseases in the spinal cord, thyroid gland, heart, CC growth abnormalities, and alleviation of precocious puberty. The coff the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder
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19-MAR-2001;
04-APR-2001;
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20-DEC-2000;
09-JAN-2001;
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Human drug metabolising enzyme (DME-10) cDNA
                                                         AAD40574;
                                                                                    AAD40574 standard; cDNA;
                             (first
                            entry)
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Human; drug metabolising enzyme; autoimmune; inflammatory disorder; acquired immunedeficiency syndrome; AIDS; atherosclerosis; psoriasis; proliferative disorder; arteriosclerosis; cirrhosis; hepatitis; cancer; asthma; neurological disorder; Alzheimer's disease; Huntington's disease; dementia; Parkinson's disease; developmental disorder; anaemia; adenoma; drug screening; endocrine disorder; conjunctivitis; glaucoma; cataract; renal tubular acidosis; eye disorder; conjunctivitis; peptic ulcer; anorexia; metabolic disorder; pstic fibrosis; diabetes; liver disorder; goitre; gastrointestinal disorder; gene therapy; virucide; anticoagulant; anticonvulsant; nootropic; enzyme; DME-10; gene; ss.

sapiens

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WO200246426-A2
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밁 ઇ 음 성

음 중

문 ঠ 밁 ક 밁 ঠ 밁 ঠ 밁 ঠ 문 ર્શ

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The invention relates to an isolated human drug metabolising enzyme (DME) and its nucleotide. DME is useful for diagnosing, treating or preventing CC disorders associated with aberrant expression of DME, where the disorders are selected from autoimmune/inflammatory disorder such as acquired CC immunodeficiency syndrome (AIDS), asthma, atherosclerosis, psoriasis, cuveitis; a cell proliferative disorder such as arteriosclerosis, proliferative disorder such as arteriosclerosis, cc already, huntington's disease, dementia, Parkinson's disease; and relevelopmental disorder such as renal tubular acidosis, epilepsy, cc anaemia; an endocrine disorder such as adenoma, thrombosis and infections in an eye disorder such as conjunctivitis, glaucoma, cataract; metabolic disorder such as anorexia, peptic ulcer; and goitre; a gastrointestinal cc disorder such as anorexia, peptic ulcer; and liver disorders. DME is cuseful in a number of drug screening techniques and to analyse the corteome of a tissue or cell type. The invention is useful for creating knock-in humanised animals or transgenic animals to model human diseases, classue or cell type. The invention is useful for creating constance or cell type, for detecting differences in the chromosomal coartier or affected individuals, and as hybridisation probes for mapping naturally occurring genomic sequences. The present sequence is human DME-10 cDNA xx
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Best Local
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Lee EA, Ding L, Ha
Lal PG, Warren BA,
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15-DEC-2000; 2000US-0256189P
21-DEC-2000; 2000US-0257713P
19-JAN-2001; 2001US-0267706P
02-FEB-2001; 2001US-0266020P
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P-PSDB; AAE25025.
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, Hafalia AJA, Tang YT, Yue H, Tribouley
BA, Yang J, Walia NK, Nguyen DB, Gandhi
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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated
                                                                                                                                                                                                                                                   New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy o
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Matches 1656;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2229 BP; 503 A; 585 C; 547 G; 594 T; 0 U; 0 Other;
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                           GGCCCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAA
                                                                              CAAAGGCTTATTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGA
                                                                                                                                        CATCTTTGGCGAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGC
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       Human; 88; gene; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction-related protein; transcription-related osteoporosis; neurological disease; cancer; tumour.
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                                                                                                            ADB62095;
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CCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG 270 GTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCCTTTGCTGCT

258 211 198 151 138 91

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Query Match Best Local Sim Matches 1653;

Similarity 99.: 53; Conservative

93.4%;

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Gaps

Score 1631.2; Pred. No. 0; 0; Mismatches

Sequence 2092 BP; 464 A; 552 C; 497

ଜ 579

T; 0 U; DB 10; ω •

0 Other; Length 2092;

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The invention discloses a polymucleotide comprising a sequence selected CC from 1970 fully defined nucleotide sequences which encode novel CC polypeptides. Also claimed is a polypeptide encoded by the polymucleotide CC or its partial paptide, an antibody binding to the polypeptide or peptide CC of the polymucleotide, immunologically assaying the polypeptide or peptide CC paptide of the polymucleotide by contacting the polypeptide or peptide CC with the antibody of the encoded protein, and observing the binding CC expressible manner and an antisense polymucleotide. The oligonucleotide in an CC expressible manner for synthesising the polymucleotide, or as a probe CC is useful as a primer for synthesising the polymucleotide, or as a probe CC proteins are useful as pharmaceutical agents and many disease-related CC genes may be included in them, for developing a diagnostic marker or CC of gene therapy. The genes are involved in tissue and/or cell consciption-related proteins, signal transduction-related proteins, concer, tumours, signal transduction-related proteins, concer, tumours. The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence presented is a cDNA of the invention. Note: Some of the sequence data for this patent is not represented in the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page; 222pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides and polypeptides, useful for developing marker or medicines for regulation of their expression and \epsilon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as targets of gene therapy.
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P-PSDB; ADB64065.
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25-JAN-2002;
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/product= "Clone BRAWH20021910 protein"
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Otsuka M, Nagahari K, Masuho Y;
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                                                                                                                 CTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAGTA
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          ATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTTCGGCACCGGCCTCAGTG
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                             CACCATCCCCTGATCCTGTCTGCCTCCGACATGCTCCACAGTCCTCTTTCCTTAAC
                                      CACCATCCCCCTGATCCTGTCTGCCTCCGACATGCTCCACAGTCCTCTTTCCTTACC
                                                          GGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGTGGATTTTTGGACCAG
                                                                                       GAAGTTACTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACCGGGAATCC
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ABX72267 standard;

CDNA; 1746 BP

ABX72267;

Human 03-JUN-2003 XVON polymucleotide (first entry. #98

RESULT 7
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AS Human; NOVX; gene; 88; metabolic disorder; cardiomyopathy; diabetes; ASI hypertension; congenital heart defect; aortic stenosis; valve disease; atrial septal defect; atrioventricular canal defect; ductus arteriosus; pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD; tuberous sclerosis; scleroderma; atherosclerosis; infectious disease; obesity; anorexia; neurodegenerative disorder; Alzheimer's disease; parkinson's disease; immune disorder; haematopoietic disorder; haemophilia; hypercoagulation; Crohn's disease;

Homo sapiens.

WO200281498-A2

17-OCT-2002

03-APR-2002; 2002WO-US010780.

03-APR-2001; 03-APR-2001; 05-APR-2001; 05-APR-2001; 06-APR-2001; 10-APR-2001; 11-APR-2001; 12-APR-2001; 13-APR-2001; 13-APR-2001; 20-APR-2001; 20-APR-2001; 23-APR-2001; 23-APR-2001; 24-APR-2001; 24-APR-2001; 2001US-0281086P.
2001US-0281136P.
2001US-0281863P.
2001US-0281906P.
2001US-0282930P.
2001US-0282934P.
2001US-0283710P.
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2001US-0283718P.
2001US-0285381P.
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2001US-0285890P.
2001US-02866880P.
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human polypeptides, termed NOVX, and the polypucleotides encoding them. The polypeptides and polypucleotides are useful for diagnosing disease, and screening for potential therapeutic agents. The sequences are useful for treating metabolic disorders, cardiomyopathy, diabetes, hypertension, congenital heart defects, articles attrials septal defect (ASD), attriaventricular canal defect, ductus arteriosus, pulmonary stenosis, subacrtic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, atherosclerosis, obesity, infectious disease, ancrexia, neurodegenerative disorders, Alzhelmer's disease, Parkinson's disease, immune disorders, haematopoietic disorders, haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease polynucleotides of the invention
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22-MAY-2001;
29-MAY-2001;
30-MAY-2001;
18-JUN-2001;
19-JUN-2001;
12-SEP-2001;
25-SEP-2001;
25-SEP-2001;
25-SEP-2001;
17-OCT-2001;
14-NOV-2001;
15-JAN-2002;
02-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated NOVX polypeptide useful for treating atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guo X, Kekuda R, Miller CE, Malyankar UM, Spytek KA; Patturajan M, Liu X, Gusev VY, Li L, Vernet CAM, Zerhusen BD; Gorman L, Shenoy SG, Pena CEA, Smithson G, Burgess CE, Gerlach v Padigaru M, Shimkets RA, Gangolli EA, Taupier RJ, Casman SJ, Ji Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ; Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA; Ellerman K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
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           GGATAACTTGCGAGAAGCCACCTCCTACCCCTAATTTGTGCCTCCAGAACTCAGAGTGGCT
                                                                    CTTTGCTGCTCCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCTG
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2001US-03124800P.
2001US-0324800P.
2001US-0324802P.
2001US-03324802P.
2001US-0332131P.
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2001US-0332175P.
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2001US-033215P.
2001US-0332175P.
2001US-0332175P.
2002US-0350251P.
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                                                         ACTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTATGAGTTTTCG
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09-JAN-2001;
30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             wound healing disorders; atherosclerosis; Parkinson's disease; Alzheimer's disease; autoimmune disorder; haematopoietic disorder; inflammation; neoplastic disease; nervous system disorder; cardiovascular disorders; pancreatitis; respiratory disorder; hyperproliferation; systemic autoimmune disease; hyper-immunity; developmental abnormality; gastrointestinal ulceration; neuropathy; haematological disease; metabolic disease; sperm dysfunction; thyroid disorder; hypothyroidism; brain damage; colitis; cone photo- transduction deficiency; neurological disease; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nootropic; neuroprotective; immunosuppressive; haemostatic; antiinflammatory; cardiant; antiulcer; virucide; antithyroid; cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                         angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;
trachea; thymus; lymph node; muscular system; obesity; anorexia;
growth abnormality; precocious puberty; gene; ss.
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Agarwal P, B
Martensen SA,
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19-MAR-2001;
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SMITHKLINE
GLAXO GROUP
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2001US-026492P.
2001US-026492P.
2001US-026692P.
2001US-0266797P.
2001US-021555P.
2001US-0281555P.
2001US-0289622P.
 Birkeland M,
A, Rizvi SK,
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Cogswell JP, Kabnick
Smith RF, Strum JC,
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Matches 1494;
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P-PSDB;
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Pred. No. 0;
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Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder
Claim 2(a); Page 251-252; 335pp; English.
                                                                                                         infection, autoimmune disorder
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The invention relates to an isolated polypeptide with signal sequences which allow it to be secreted extracellularly or membrane associated. The contivity of polypeptides of the invention may be described as, contivity of polypeptides of the invention may be described as, concerning the continuous continuous pressive, haemostatic, antiparkinsonian, nootropic, continuous continuous cardiant, antiulcer, virucide, antithyroid, cerebroprotective, amorectic, cardiant, antiulcer, virucide, antithyroid, cerebroprotective, amorectic, cand metabolic. Polypeptides and polynucleotides of the invention are considered in the treatment, or as a vaccine in the prevention of, cancer, consequently disorders, infection, atherosclerosis, Parkinson's disease and Alzheimer's disease, anticimmune disorder, haematopoietic disorder, cand alzheimer's disease, anticimmune disorder, haematopoietic disorders and cardiovascular disorders, pancreatitis, respiratory disorder, confidently, continuous system related disorders and cardiovascular abnormality, gastrointestinal ulceration, neuropathy, continuous diseases, hyper-immunity, continuous diseases, metabolic diseases, sperm dysfunction, thyroid disorders e.g. hypothyroidism, brain damages, colitis, cone photocontinuous disorders, diseases in the spinal cord, thyroid gland, heart, convolation disorders, diseases in the spinal cord, thyroid gland, heart, convolation disorders, and alleviation of precocious puberty. The sequences given in records ABQ86130-ABQ86184 represent novel human cDNA's

Sequence 1746 BP; 401 A; 464 C; 459 G; 422 T; 0 U; 0 Other;

DB 6;

Indels Length

21;

Gaps

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GTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCCTTTGCTGCT
ACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCC
                                                                                                                                                     CCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCC
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                                                      TATGAGGACGTGCTGGTGGTCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACC
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                                                                                                             ACGGAGGAGGAGATTACTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCTCGA
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TTTTGG 1635
                            TACCTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGAGAGAT
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22-NOV-2000; 2000US-0252834P.
30-NOV-2000; 2000US-0250567P.
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Azimzai Y, Elliott VS, Lal P, Lee Ring HZ, Sa Human drug metabolizing enzymes, useful idisorders associated with aberrant (DME) autoimmune disorders. Walsh 2002-362498/39. DB; ADR19663. ii Y, Baughin MR, But VS, Gandhi AR, GL Lee EA, Lu DAM, II IZ, Sanjanwala MS, II Borowsky ML, Ding L, Duggan BM; Griffin JA, Hafalia AJA, Igon CH, K Nguyen DB, Arvizu C, Policky JL, R, Tang YT, Tribouley CM, Narinder WK; u Y, Yang J, Yao MG, Yue H; in the diagnosis and treatment activity, e.g., cancer and Khan Ö. 4

Claim 12; SEQ ID NO 20; 142pp; English.

This invention relates to novel drug metabolising enzymes (DME) and the nucleotide sequences which encode them. The invention may be useful for the development of compounds with a cytostatic, immunosuppressive, antiinflammatory, endocrine, ophthalmological, gastrointestinal or hepatotropic activity acting as an agonist or antagonist of drug metabolising enzyme activity. The invention may be used in the diagnosis and treatment of disorders associated with decreased or increased expression or activity of drug metabolising enzymes. Such disorders include cancer, cell proliferative disorders, autoimmune/inflammatory, endocrine, eye, gastrointestinal (including liver disorders) and metabolic disorders. The present sequence is that of a gene which encodes a human drug metabolising enzyme (DME) of the invention. Note: This sequence did not form part of the printed specification but was obtained in electronic format from EPO.

1857 BP; ð, 487 ü 446 H 0 ₽ 0

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                      CATCTTTGGCGAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGC
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Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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                                             WPI; 2003-395539/38
P-PSDB; ADA54807.
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24-JAN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human coding sequence, SEQ ID
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The present sequence encodes a cat cauxin protein (I) or its salt, which CC is cat kidney disease marker. Also described: (I) a partial peptide (II) cof (I); (2) a nucleic acid (III) encoding (I) or (II); (3) a vector (IV) CC comprising (III); (4) a transformed host (V) comprising (III) or (IV); (C comprising (III)) or (II) by culturing (V); (6) a antibody (VI) which CC couples specifically with (I) or (II); (7) diagnosing cat kidney disease CC which involves measuring (I) quantitatively, and where reduction of CC amount of (I) indicates presence of the disease; (8) a cat kidney disease CC diagnostic agent comprising (I) labelling agent, a reagent which measures CC the biological activity of urinary (I) or (VI); and (9) a cauxin CC cat kidney disease marker and (VI) is useful for diagnosing cat kidney CC disease. (I) provides an early marker for the disease, and replaces CC complicated diagnostic methods such as X-ray imaging, ultrasonic imaging,
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Best Local Similarity
Matches 1329; Conserv
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Best Local Similarity
Matches 1265; Conserv
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                                     AGAGATGCTGGTGCACCTGTCTATGAGTTTCAACACCCGCCCCAGTGCTTAAAC 1320
                                                                             AGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTTCGGCACCGGCCTCAGTGCTTTGAA 1347
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20-DEC-2000;
09-JAN-2001;
30-JAN-2001;
06-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences given in records ABQ86130-ABQ86184 represent novel human cDNA's of the invention
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     CTGACTGAAATCCGAGACAGTCTTCTGGACTTGCTTGGAGATGTGTTCTTTGTGGTCCCT 1263
                                                                                          CACATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAGCACTCC 1203
                                                                                                                                                                                                   CCTGAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCCCTCCATCTGATACAAAACATCCTG
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                                                           CACATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAGCACTCC
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WPI; 2003-269506/27.
P-PSDB; ADC55524.
                       Mao Y,
                                                   26-APR-2001; 2001CN-00112736
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                                                                                  04-DEC-2002
                                                                                                 CN1382799-A
                                                                                                                                                          human carboxylatase-24.64; primary hypertension; nephrotic; bronchial asthma; gene; ss.
                                                                                                                                                                               Human carboxylatase 24.64 encoding sequence
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Claim 6; SEQ ID NO 1; 31pp; Chinese.
                              Polypeptide-human carboxylatase-24.64 and
                              polynucleotide
                              for
                             coding
                              it.
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The present invention relates to a polypeptide-human carboxylatase-24.64, the polymucleotide for coding it, the process for preparing the polypeptide by DNA recombination, the application of the polypeptide in treating diseases such as primary hypertension, digestive ulcer, nephrotic, bronchial asthma, tremor, etc, the antagon of the polypeptide and its medical action, and the application of the polynucleotide are new. The present sequence represents human carboxylatase 24.64 encoding

Sequence 1244 BP; 301 A; 314 C; 271 G; 358 T; 0 U; 0 Other;

Query Match

Local

Similarity

51.8%; 99.7%;

Length

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                                                  TCTGACTGAGCAGTACCTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGACTCAAAGA 1616
                                                                                                                TACCTTTGCTCGAACCGGGAATCCTAATGGGAACGACCTGTCTCTGTGGCCAGCTTATAA 1556
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Pred. No. 1.4e-256;
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The invention relates to a purified human carboxylesterase-like enzyme CC polypeptide. Carboxylesterase-like enzyme and its DNA are useful for CC screening for agents which decrease or modulate the activity of CC carboxylesterase-like enzyme polypeptide. Carboxylesterase-like enzyme is useful for treating a carboxylesterase-like enzyme dysfunction related CC disease, such as organophosphorus intoxication, cancer and osteoporosis. CC Compounds that increase the ability of human carboxylesterase-like enzyme to bind to organophosphorus compounds are useful as detoxifying agents. CC Carboxylesterase-like enzyme agonists and antagonists are useful for CC treating osteoporosis, Paget's disease and degradation of bone implants, CC particularly dental implants. Carboxylesterase-like enzyme is useful in CC diagnostic assays for detecting diseases and abnormalities or CC susceptibility to diseases or abnormalities related to the presence of carboxylesterase-like enzyme. The CC coding sequence of carboxylesterase-like enzyme polymucleotide is useful cin gene therapy and for generating antisense oligonucleotides or cribozymes which specifically bind to mRNA transcribed from CC carboxylesterase-like enzyme DNA. These antisense oligonucleotides are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; carboxylesterase-like enzyme; organophosphorus intoxication; gen osteopathic; gene therapy; osteoporosis; antisense therapy; cytostatic; detoxifying agent, Paget's disease; bone implant degradation; cancer; dental implant; enzyme; gene expression; ss.
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                    CAGCTCGATATCACAGAGATG 1294
                                                         TCCGAGACAGTCTTCTGGACTTGCTTGGAGATGTGTTCTTTTGTGGTCCCTGCACTGATCA
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                                           TCCGAGACAGTCTTCTGGACTTGCTTGGAGATGTGTTCTTTGTGATCCCTAAGCTGATCA
                                                                                       TCAGTGGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAACATCCTGCACATCCCGC 1153
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Search completed: June 14, 2005, 18:10:11 Job time: 944.402 secs



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Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -MODEL=frame+ n2p.model -DEV=xlh
-Q=/cgn2 1/USPTO spool/6664091/runat 14062005 133458 9325/app query.fasta 1.4238
-DB=A Geneseq 16Dec04 -QFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -STRART=1 -END=-1 -WATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -WORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=664091 @CCM 1 299 @runat 14062005 133458 9325 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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1: genesecm19anc.*
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10633.187 Million cell updates/sec
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ABP61005
ADA54807
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Human pro
Human Nov
Human pro
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1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1179.5	1181	1186.5	1191	1213.5	1221	1230	1230	1230	1230	1230	1230	1230		1780	8	8
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ABU81549	ABU67116	ABU82152	AB025111	ABU69085	ABU59921	ABU66840	ABO19424	ABU81140	ABO33809	ABU80843	ABU69108	ABO17886	ABG64341	ABB84949	AAU83696	AAE04101	AAU12442	AAY71107	ABG10273	ADI79890	ABU53222	ADD46519	AAE20909	ADD46521	AAE33960	ABB82851	ABU53223	AAB31700	ADG98219		AAE20911	6100	F5014	ADF50145 ·
Abu81549 Human sec	7116	Abu82152 Novel hum	Abo25111 Human sec	v	Abu59921 Novel sec	Human	Abo19424 Human sec	Human			Human		Human	Human	Human	Human	Human	Human	Novel	Mouse	Huma	Rat Pi	Huma	Add46521 Human Pro	Aae33960 Human car	Abb82851 CES2 rela	Abu53223 Human met	Aab31700 Protein e			2	σ	50147 Cat	Adf50145 Cat cauxi

ALIGNMENTS

Human carboxylesterase family member 53010.

23-SEP-2002 ABB79537;

(first entry)

ABB79537 standard; protein;

581 AA

Carboxylesterase; enzyme; human; analgesic; nootropic; antiinflammatory;

diagnosis; therapy.

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RESULT 1
ABB79537
ID ABB7
XX ABB7
XX ABB7
XX ABB7
XX Carb
DR Huma
XX Carb
KW Ciab
COS Homo
XX Homo
XX Homo
XX Homo
XX Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the protein sequence of human 53010, a novel C protein containing the structural characteristics of a carboxylesterase CC family member. The invention provides 53010 nucleic acids, antisense CC molecules, expression vectors, host cells, transgenic animals, 53010 CC proteins, fusion proteins, antigenic peptides, anti-53010 antibodies and CC methods for detecting the presence of 53010 polypeptides or nucleic acids, of identifying a compound that binds to the 53010 polypeptide, and CC controlling the activity of the polypeptide. The 53010 polypeptide and CC nucleic acids can act as novel diagnostic and therapeutic agents for CC controlling disorders involving aberrant or deficient hydrolysis of CC carboxylic esters. As 53010 mRNA is highly expressed in the central and CC pain models, 53010 molecules can also act as novel diagnostic targets and CC therapeutic agents for controlling neurological disorders, such as pain-CC related disorders. A claimed method of treating or preventing a disorder CC of a 53010 expressing cell involves administering a compound that CC modulates 53010 activity or expression
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The present invention describes the use of polypeptides related to urological disorders for identifying a compound capable of treating a urological disorder, identifying a subject having a urological disorder, or treating a subject having a urological disorder. Also described: (1) method for identifying a compound capable of treating a urological disorder; (2) a method for identifying a subject having a urological
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Matches:
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cerebroprotective; anorectic; metabolic; vaccine; cancer; Infection; wound healing disorders; atheroselerosis; Parkinson's disease; Alzheimer's disease; autoimmune disorder; haematopoietic disorder; Alzheimer's disease; autoimmune disorder; haematopoietic disorder; cardiovascular disorders; pancreatitis; respiratory disorder; cardiovascular disorders; pancreatitis; respiratory disorder; hyperproliferation; systemic autoimmune disease; hyper-immunity; developmental abnormality; gastrointestinal ulceration; neuropathy; developmental abnormality; gastrointestinal ulceration; neuropathy; heamatological disease; metabolic disease; sperm dysfunction; thyroid disorder; hypothyroidism; brain damage; colitis; cone photo- transduction deficiency; neurological disease; stroke; angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart; trachea; thymus; lymph node; muscular system; obesity; anorexia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nootropic; neuroprotective; immunosuppressive; haemostatic; antiinflammatory; cardiant; antiulcer; virucide; antithyroid;
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Homo

growth abnormality; precocious puberty

WO200250105-A1

27-JUN-2002

17-DEC-2001; 2001WO-US049232

19-DEC-2000; 2000US-0256710P.
20-DEC-2000; 2000US-0257048P.
09-JAN-2001; 2001US-026492P.
30-JAN-2001; 2001US-026492P.
06-FEB-2001; 2001US-0266797P.
19-MAR-2001; 2001US-0276988P.
04-APR-2001; 2001US-0281535P.
08-MAY-2001; 2001US-0289622P.

(SMIK) Agarwal P, SMITHKLINE BEECHAM CORP SMITHKLINE BEECHAM PLC. GLAXO GROUP LTD. SA, Birkeland M, A, Rizvi SK, Cogswell JP, Kabnick KF, Smith RF, Strum JC, Xie Ö

N-PSDB; WPI; 2002-508784/54. DB; ABQ86169.

Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.

Claim 1(a); Page 312-313; 335pp; English.

The invention relates to an isolated polypeptide with signal sequences CC which allow it to be secreted extracellularly or membrane associated. The CC activity of polypeptides of the invention may be described as, CC cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic, CC neuroprotective, immunosuppressive, haemostatic, antiinflammatory, CC cardiant, antiulcer, virucide, antityroid, cerebroprotective, anorectic, and metabolic. Polypeptides and polynucleotides of the invention are CC useful in the treatment, or as a vaccine in the prevention of, cancer, CC wound hashing disorders, infection, atherosclerosis, Parkinson's disease and hlzheimer's disease, autoimmune disorder, haematopoietic disorder, inflammation, neoplastic diseases, nervous system related disorders, and CC cardiovascular disorders, pancreatitis, respiratory disorder, CC hyperproliferation, systemic autoimmune disease, hyper-immunity, CC developmental abnormality, gastrointestinal ulceration, neuropathy, CC developmental abnormality, asstrointestinal ulceration, thyroid disorders e.g. hypothyroidism, brain damages, colitis, cone photo-cc transduction deficiency, neurological diseases, stroke, angiogenesis,

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ABP61004 standard;

protein; 575

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Human; drug metabolising enzyme; autoimmune; inflammatory disorder; acquired immunedeficiency syndrome; AIDS; atherosclerosis; psoriasis;
                      Human drug metabolising enzyme (DME-10).
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                                                                                                                                    LysProAlaPheValLysAlaAspHisAlaAspGluValArgPheValPheGlyGlyAla
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proliferative disorder; arteriosclerosis; cirrhosis; hepatitis; cancer; asthma; neurological disorder; Alzheimer's disease; Huntington's disease; dementia; Parkinson's disease; developmental disorder; anaemia; adenoma; drug screening; endocrine disorder; conjunctivitis; glaucoma; cataract; renal tubular acidosis; eye disorder; epilepsy; thrombosis; peptic ulcer; anorexia; metabolic disorder; cystic fibrosis; diabetes; liver disorder; goitre; gastrointestinal disorder; gene therapy; virucide; anticoagulant; anticonvulsant; nootropic; enzyme; DME-10. Homo sapiens.

WO200246426-A2 Domain Domain Domain Domain Domain Peptide note= note= 'note= 113. .135 /note= notes /label= Signal_peptide 32. .56 location/Qualifiers note= .642 .314 .250 "Transmembrane "Transmembrane "Transmembrane domain" "Transmembrane "Transmembrane domain" "Transmembrane domain" "Mature human DME-10" domain" domain" domain"

13-JUN-2002.

04-DEC-2001; 2001WO-US047429

08-DEC-2000; 2000US-025430BP. 15-DEC-2000; 2000US-0256189P. 21-DEC-2000; 2000US-0257713P. 19-JAN-2001; 2001US-0262706P. 02-FEB-2001; 2001US-0266020P.

(INCY-) INCYTE GENOMICS INC.

Lee EA, Lal PG, Ison CH; Sanjanwala MM, la MM, Yao MG, Au-Young J, Baughn MR, Arvizu C, Ding L, Hafalia AJA, Tang YT, Yue H, Tribouley Warren BA, Yang J, Walla NK, Nguyen DB, Gandhi Ring HZ; CM, Lu D AR, Lu Y

WPI; 2002-519668/55. N-PSDB; AAD40574.

Novel human drug metabolizing polypeptide, useful in diagnosis, prevention or treatment of autoimmune/inflammatory, cell proliferative neurological; developmental, endocrine, metabolic and gastrointestinal

Claim 65; Page 155-156; 169pp; English.

The invention relates to an isolated human drug metabolising enzyme (DME) CC and its nucleotide. DME is useful for diagnosing, treating or preventing cd disorders associated with aberrant expression of DME, where the disorders commune/inflammatory disorder such as acquired immunedficiency syndrome (AIDS), asthma, atherosclerosis, psoriasis, curveitis; a cell proliferative disorder such as arteriosclerosis, people cc uveitis; a cell proliferative disorder such as arteriosclerosis, cc cirrhosis, hepatitis, and cancer; a neurological disorder such as cc advelopmental disorder such as renal tubular acidosis, epilepsy, cc alevelopmental disorder such as renal tubular acidosis, epilepsy, cc anaemia; an endocrine disorder such as adenoma, thrombosis and infections cr an eye disorder such as conjunctivitis, glaucoma, cataract; metabolic clisorder such as cystic fibrosis, diabetes and goitre; a gastrointestinal cc disorder such as cystic fibrosis, diabetes and goitre; a gastrointestinal cc useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. The invention is useful for creating

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Ş	D Qy	D Q	в <i>Q</i>	B &	₽ Q	B &	B 8	B 8	B &	р Q	B &	D Q	d Q	US-10-	Alignmer Pred. No Score: Percent Best Loc Query Ma DB:	೧೧೧೧೧೧೮೮೮
871 TCTGAGGCCCTGAGGTGCCTGAGGACAAAACCCTCCAAGGAGCTGCTGACCCTCAGC 930	811 TATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAATGCGTCAGAC 870 	751 TTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGAGGCCCATGAT 810	2	631 TGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGC 690 	571 ACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCC 630		451 CCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCC 510	391 AACATCTATGCGCCTGCCCACGCCGATACAGGCTCCCAAGCTCCCCGTCTTGGTGTGTTC 450 	331 CAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTG 390 	271 CGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGAT 330	211 CCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG 270 	151 GTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCCTTTGCTGCT 210	91 GGGCCTTCTGCTGAAGGGCCACAGAGGAACACCAGGCTGGGATTGAATTCAGGGCAAGCAA	-023-515-3 (1-1746) x AAE25025 (1-642)	ignment Scores: 6.21e-270 Length: 642 ad. No.: 2900.00 Matches: 548 crent Similarity: 99.82% Conservative: 2 crent Similarity: 99.46% Mismatches: 1 st Local Similarity: 99.46% Mismatches: 1 ary Match: 91.48% Indels: 0 ary Match: 5 Gaps: 0	knock-in humanised animals or transgenic animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in the chromosomal location due to translocation, inversion, etc. among normal, carrier or affected individuals, and as hybridisation probes for mapping naturally occurring genomic sequences. The present sequence is human DME-10 Sequence 642 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel diagnostic and therapeutic polynucleotides CC selected from one of the 2722 sequences defined in the specification. A CC polynucleotide of the invention may have a use in gene therapy. The human CC diagnostic and therapeutic polynucleotides (dithp) or polypoptides may be used to diagnose a particular condition, disease or disorder associated CC with human molecules, e.g. cell proliferative disorder, endocrine autoimmune/inflammatory disorders, developmental disorder, endocrine CC disorder, neurological disorders, gastrointestinal disorders, or CC infections caused by virus, bacteria, fungi or parasite. The dithp CC molecules may also be used in genetic mapping, in identifying individuals CC from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline CC invention. Note: The sequence represents a dithp protein of the CC invention. Note: The sequence data for this patent is not represented in CC the printed specification, but was obtained in electronic format directly cycles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralle CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzer
Patury S, Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
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N-PSDB; ACN42766.
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12-SEP-2002;
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20-DEC-2000;
09-JAN-2001;
30-JAN-2001;
06-FEB-2001;
19-MAR-2001;
04-APR-2001;
08-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated polypeptide with signal sequences CC which allow it to be secreted extracellularly or membrane associated. The CC extrict of polypeptides of the invention may be described as, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic, neuroprotective, immunosuppressive, haemostatic, antiinflammatory, CC cardiant, antiulcer, virucide, antithyroid, cerebroprotective, anorectic, and metabolic. Polypeptides and polymucleotides of the invention are useful in the treatment, or as a vaccine in the prevention of, cancer, CC wound healing disorders, infection, atherosclerosis, Parkinson's disease and polymucleotides, harkinson's disease, autoimmune disorder, haematopoietic disorder, inflammation, neoplastic diseases, nervous system related disorders and cardiovascular disease, autoimmune disorder, haematopoietic disorders and CC dardiovascular disorders, pancreatitis, respiratory disorder, hyperproliferation, systemic autoimmune disease, hyper-immunity, CC developmental abnormality, gastrointestinal ulceration, neuropathy, haematological diseases, metabolic diseases, sperm dysfunction, thyroid disorders e.g. hypothyroidism, brain damages, colitis, cone phototraschea, thymus, hypothyroidism, brain damages, colitis, cone phototraschea, thymus, lymph node and muscular system, obesity; anorexia, CC trachea, thymus, lymph node and muscular system, obesity; anorexia, CC trachea, thymus, lymph node and muscular system, obesity; anorexia, CC proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder
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                                                                                                          ProGlnCysPheGluAspThrLysProAlaPheValLysAlaAspHisAlaAspGluVal
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Yamamoto J,
Seki N, You
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                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                             hypertension; congenital heart defect; aortic stenosis; valve disease; atrial septal defect; atrioventricular canal defect; ductus arreriosus; pulmonary stenosis; subaortic stenosis; ventricular septal defect; VSD; tuberous selerosis; seleroderma; atherosclerosis; infectious disease; obesity; anorexia; neurodegenerative disorder; Alzheimer's disease; parkinson's disease; immune disorder; haematopoietic disorder;
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2001US-0281863P.
2001US-0281906P.
2001US-0282020P.
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Guo X, Kekuda R, Miller CE, Malyankar UM, Spytek KA; Patturajan M, Liu X, Gusev VY, Li L, Vernet CAM, Zerhusen BD; Gorman L, Shenoy SG, Pena CEA, Serhoson G, Bergess CE, Gerlaci Padigaru M, Shimkete RA, Gangolli EA, Taupier RJ, Casman SJ, Anderson DW, Leite MW, Rastelli L, Edinger SR, Stone DJ; Macdougall JR, Rothenberg ME, Mazur A, Millet I, Peyman JA; <u>~</u> χ.,

N-PSDB; WPI; 2003-046858/04. ABX72267.

New isolated NOVX polypeptide useful for treating atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease and cancer.

Claim 1; Page 303; 666pp; English.

The invention relates to human polypeptides, termed NOVX, and the polypurcleotides encoding them. The polypeptides and polynucleotides are useful for diagnosing disease, and screening for potential therapeutic agents. The sequences are useful for treating metabolic disorders, cardiomyopathy, diabetes, hypertension, congenital heart defects, action attrial septal defect (ASD), attrioventricular canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, atherosclerosis, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, immune disorders, haematopoietic disorders, haemophilia, hypercoagulation, Crohn's disease and cancer. Sequences ABUS4542-ABUS4647 represent human NOVX polypeptides and cancer. of the inver invention

Sequence 581

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                     29-SEP-2000;
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09-NOV-2000;
16-NOV-2000;
22-NOV-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                         drug metabolising enzyme; DME; cytostatic; immunosuppressive; antiinflammatory; endocrine; ophthalmological; strointestinal; hepatotropic; cancer; cell proliferative disorder; autoimmune disorder; inflammatory disorder; endocrine disorder; eye disorder; gastrointestinal disorder; liver disorder; metabolic disorder; enzyme;
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Qy 211 CCCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG 270	Gaps: 023-515-3 (1-1746) x ADR19663 (1-618) 91 GGGCCTTCTGCTGAAGGGCCACAGAGGAACACCAGGCTGG	eg		Azimzai Y, Baughin MR, Borowsky ML, Ding L, Duggan BM; PI Rilliott VS, Gandhi AR, Griffin JA, Hafalia AJA, Ison CH, Khan FA; PI Elliott VS, Gandahi AR, Griffin JA, Hafalia AJA, Ison CH, Khan FA; PI Lal P, Lee EA, Lu DAM, Nguyen DB, Arvizu C, Policky JL, Ramkumar J; PI Ring HZ, Sanjanwala MS, Tang YT, Tribouley CM, Narinder WK; PI Walsh RT, Warren BA, Xu Y, Yang J, Yao MG, Yue H; XX WPI; 2002-362498/39. DR WPI; 2002-362498/39. DR N-PSDB; ADR19681. XX Human drug metabolizing enzymes, useful in the diagnosis and treatment of disorders associated with aberrant (DME) activity, e.g., cancer and PT autoimmune disorders. XX Claim 1; SEQ ID NO 2; 142pp; English.
				
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Alignment Scores: 
Pred. No.:
                                                                                The invention discloses a polymucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel control of the polymucleotide, an antibody binding to the polymucleotide or peptide or peptide or peptide of the polymucleotide, immunologically assaying the polypeptide or peptide of the polymucleotide, immunologically assaying the polypeptide or peptide of the polymucleotide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding compared the two, a transformant carrying the polymucleotide in an expressible manner and an antisense polymucleotide. The oligonucleotide is useful as a primer for synthesising the polymucleotide, or as a probe contacting the polymucleotide and encoded contacting the polymucleotide and encoded contacting the polymucleotide and encoded contacting the polymucleotide and encoded contacting the polymucleotide and encoded contacting the polymucleotide and encoded contacting the polymucleotide and encoded contactines for regulation of their expression and activity, or as targets confidence in the proteins, signal transduction-related proteins, disease-related proteins and genes are involved in tissue and/or cell contacting them can be used as indicators for diseases (e.g. osteoporosis, encoding them can be used as indicators for diseases (e.g. osteoporosis, concervitually or expression of the encoded protein to treat diseases. The sequence presented is a protein of the invention. Note: Some of the sequence data for this patent is not represented in the printed concervitual patent is based on sequence information supplied by the concervitual patent of encoded protein the printed concervitual patent is a protein of the invention.
                                                  Sequence 469
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Yamamoto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-450961/43.
N-PSDB; ADB62095.
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25-JAN-2002; 2002US-00350978.
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T, Isono Y,
Yoshikawa T,
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Hio Y, Otsuka K, Nagai K,
Otsuka M, Nagahari K, Masu
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GGTGCACCTGTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTGCTTTGAAGACACGAAG 1356
                         CTTGGAGATGTGTTCTTTGTGGTCCCTGCACTGATCACAGCTCGATATCACAGAGATGCT 1296
                                                                                                                AATGAATACTTCCATGACAAGCACTCCCTGACTGAAATCCGAGACAGTCTTCTGGACTTG
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The present sequence represents a cat cauxin protein (I) or its salt, which is cat kidney disease marker. Also described: (I) a partial peptide (II) of (I); (2) a nucleic acid (III) encoding (I) or (II); (3) a vector (IV) comprising (III); (4) a transformed host (V) comprising (III) or (IV); (5) producing (I) or (II) by culturing (V); (6) a antibody (VI) which couples specifically with (I) or (II); (7) diagnosting cat kidney disease which involves measuring (I) quantitatively, and where reduction of amount of (I) indicates presence of the disease; (8) a cat kidney disease diagnostic agent comprising (I) labelling agent, a reagent which measures the biological activity of urinary (I) or (VI); and (9) a cauxin
                                                                                                                                                                                         Novel cauxin protein or its salt, useful as and for diagnosing cat kidney disease.
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DR WPI; 2004-002277/01.

DR N-PSDB; ADF50146.

XX

PT Novel cauxin protein or its salt, useful as a cat kidney disease marker, PT and for diagnosing cat kidney disease.

XX

PT and for diagnosing cat kidney disease.

XX

PT and for diagnosing cat kidney disease.

XX

PT and for diagnosing cat kidney disease.

XX

PT and for diagnosing cat kidney disease marker. Also described: (1) or its salt, curve which is cat kidney disease marker. Also described: (1) a partial peptide (1); (2) a nucleic acid (III) encoding (I) or (II); (3) a vector (IV); (5) producing (I) or (II) by culturing (V); (6) a antibody (VI) (CI); (5) producing (I) or (II) by culturing (V); (6) a antibody (VI); (7); (8) producing (I) or (II); (7) diagnosing cat kidney (1) enables diagnostic agent comprising (I) plantitatively, and where reduction of amount of (I) indicates presence of the disease; (8) a cat kidney disease diagnostic agent comprising (I) labelling agent, a reagent which curve the biological activity of urinary (I) or (VI); and (9) a cauxin of detection kit which measures cauxin in a test sample. (I) is useful as a cat kidney disease marker and (VI) is useful for diagnosing cat kidney disease. (I) enables detection of cat kidney disease simply and correctly. (1) provides an early marker for the disease, and replaces complicated diagnostic methods such as X-ray imaging, ultrasonic imaging, XX

Sequence 542 AA;
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US-10-023-515-3 (1-1746) x ADF50147 (1-542)

Query Match: DB:

Percent Similarity: Best Local Similarity:

1e-181 1985.00 83.27% 71.73% 62.62%

Length:
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542 60 85 2

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wound healing disorders; atherosclerosis; Parkinson's disease; Alzheimer's disease; autoimmune disorder; haemaropoietic disorder; inflammation; neoplastic disease; nervous system disorder; cardiovascular disorders; pancreatitis; respiratory disorder; cardiovascular disorders; pancreatitis; respiratory disorder; hyperproliferation; systemic autoimmune disease; hyper-immunity; developmental abnormality; gastrointestinal ulceration; neuropathy; haemacological disease; metabolic disease; sperm dysfunction; thyroid disorder; hypothyroidism; brain damage; colitis; cone photo- transduction deficiency; neurological disease; stroke; angiogenesis; ovulation disorder; splnal cord; thyroid gland; heart; trachea; thymus; lymph node; muscular system; obesity; anorexia; growth abnormality; precocious puberty.
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WO200250105-A1

27-JUN-2002.

17-DEC-2001; 2001WO-US049232

19-DEC-2000; 20-DEC-2000; 09-JAN-2001; 30-JAN-2001; 06-FEB-2001; 19-MAR-2001; 04-APR-2001; 08-MAY-2001; ; 2000US-0256710P. ; 2000US-0257048P. ; 2001US-0260482P. ; 2001US-0264922P. ; 2001US-0266797P. ; 2001US-0276988P. ; 2001US-0281535P. ; 2001US-0281535P.

(SMIK) (SMIK) Agarwal P, SMITHKLINE BEECHAM SMITHKLINE BEECHAM GLAXO GROUP LTD. SA, Birkeland A, Rizvi S Cogswell JP, Kab Smith RF, Strum CORP PLC. Kabnick KF, rum JC, Xie

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2002-508784/54.

Secreted proteins and polynucleotides useful as vaccines for preventing or treating various diseases e.g. cancer, wounds, atherosclerosis, Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder autoimmune disorder

Claim 1(a); Page 315; 335pp; English.

The invention relates to an isolated polypeptide with signal sequences which allow it to be secreted extracellularly or membrane associated. The activity of polypeptides of the invention may be described as, compared to the invention may be described as, antiparkinsonian, nootropic, compared to the invention may be described as compared to the invention may be described as compared to the invention of the invention of the invention of the invention are compared to the invention are and metabolic. Polypeptides and polynucleotides of the invention are compared to the invention of

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                                                                                          GATGAAGTCCGCTTTGTGTTCCGGTGCTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAA 1443
                                                                                                              CTGACTGAAATCCGAGACAGTCTTCTGGACTTGCTTGGAGATGTGTTCTTTGTGGTCCCT
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Sequence

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RESULT 14
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                                                                                The invention relates to a purified human carboxylesterase-like enzyme CC polypeptide. Carboxylesterase-like enzyme and its DNA are useful for CC screening for agents which decrease or modulate the activity of CC carboxylesterase-like enzyme polypeptide. Carboxylesterase-like enzyme is CC carboxylesterase-like enzyme polypeptide. Carboxylesterase-like enzyme is CC carboxylesterase-like enzyme is CC compounds that increase the ability of human carboxylesterase-like enzyme CC compounds that increase the ability of human carboxylesterase-like enzyme CC carboxylesterase-like enzyme agonist are useful as detoxifying agents. CC carboxylesterase-like enzyme agonists and antagonists are useful for treating osteoporosis, Paget's disease and degradation of bone implants, CC carboxylesterase-like enzyme is useful in CC diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases or abnormalities related to the presence of coding sequence of carboxylesterase-like enzyme polynucleotide is useful in gene therapy and for generating antisense oligonucleotides or CC useful the pecifically bind to mRNA transcribed from carboxylesterase-like enzyme of carboxylesterase-like enzyme oligonucleotides are useful for modulating carboxylesterase-like enzyme oligonucleotides are useful sequence is rat carboxylesterase-like enzyme expression. The CC useful sequence is at carboxylesterase-like enzyme oligonucleotides are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human carboxylesterase-like enzyme polypeptide, regulators of which are useful for preventing and treating organophosphorus intoxication, cancer and osteoporosis.
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Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepacotropic; antidiabetic; antiinflammatory; antiucer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple solerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease.
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                                                                                                                                                                                                                       cancer associated antigen protein sequence
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                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences AAF21614 - AAF22031 represent DNA sequences encoding human CC proteins AAB58711 - AAB59128. The DNA and protein sequences are CC associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the CC isolation and characterisation of the DNA and protein sequences of the CC invention. The breast and ovarian cancer associated DNA, protein, agonist CC entragonist sequences exhibit cytostatic; immunosuppressive; nontropic; antiinflammatory; antivical; antiallergic; hepatotropic; antidiabetic; CC entiinflammatory; antivical; and cardiant activity. The polynucleotide and CC protein sequences are used in the diagnosis of cancer, particularly Drotein sequences are used in the diagnosis, prevention and treatment CC and agonists may also be used in the diagnosis, prevention and treatment CC immune disorders e.g. Addison's disease, allergies, autoimmune CC isease, multiple sclerosis, rheumatoid arthritis and ulcerative CC cardiovascular disorders such as myocardial ischaemias; wound healing; cardiovascular disorders such as cerebral anoxia and epilepsy; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                  infectious diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 1142-1144; 1299pp;
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             CACGCTGATGAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATG
GluPheGlnHisGlnProSerTrpLeuLysAsnIleArgProProHisMetLysAlaAsp
                                                                             GAGTTTCGGCACCGGCCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGAC
                                                                                                      IleProAlaLeuGlnValAlaHisPhe---GlnCysSerArgAlaProValTyrPheTyr
                                                                                                                                                          GlyAspProGlnThrLeuGlnAlaGlnPheGlnGluMetMetAlaAspSerMetPheVal
                                                                                                                                                                                                           LeuLeuMetLeuProProThrPheGlyAspLeuLeuArgGluGluTyrIleGlyAspAsn
                                                                                                                                                                                                                                    ATCCTGCACATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAG
                                                                                                                                                                                                                                                                                                                              {\tt AspThrGlnLysGluMetAspArgGluAlaSerGlnAlaAlaLeuGlnLysMetLeuThr}
                                                                                                                                                                                                                                                                                       GAGGCTCCTGAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAAC 1137
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AspCysLeuTyrLeuSerIleTyrThrProAlaHisSerHisGluGlySerAsnLeuPro
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Command line parameters:

-MODEL-frame+ n2p.model -DEV=xlh
-Q-Ggn2_1/USPTO_spool/664091/runat_14062005_133459_9346/app_query.fasta_1.4238
-DB=PIR 79 -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.I.-LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pet -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=50 -MINLEN=0 -MAXLEN=200000000
-USER=6664091_@CGN 1 101 @runat 14062005 133459 9346 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG SCORES=0 -MAIT -DSPBLOCE=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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ALIGNMENTS

thiolesterase B (EC 3.....) precursor - mallard C;Species: Anas platyrhynchos (mallard) C;Date: 05-May-1995 #sequence_revision 05-May-1995 #text_c;Caccession: A47162 R;Hwang, C.S.; Kolattukudy, P.E. J. Biol. Chem. 268, 14278-14284, 1993 A;Reference number: A47162; MUID:93300823; PMID:8314791 A;Accession: A47162; MUID:93300823; PMID:8314791 A;Accession: A47162 Ś A;Cross-references: UNIPROT:Q04791; GB:L05493; NID:g213100; PIDN:AAA49223.1; PID:g213101 C;Superfamily: cholinesterase; cholinesterase homology C;Keywords: hydrolase 밁 밁 á Percent Similarity: Best Local Similarity: A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-557 <HWA> US-10-023-515-3 (1-1746) x A47162 (1-557) Pred. No.: Alignment Scores: F;56-545/Domain: cholinesterase homology <CHE> Query Match: SCOTE: 148 CAAGTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCCTTTGCT 43 23 ThrGlyGlnLysAlaGluGlnProGluValValThrAsnTyrGlySerValArgGlyTyr 42 GlnValLysValAsnAlaAlaGluArgSerValAsnValPheLeuGlyLeuProPheAla 1.99e-92 1298.50 62.77% 48.36% 40.96% Length:
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208 GCTCCCCCCCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAAC

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                                                                                                                                                                      CTGCACATC------CCGCCTCAGTATTTGCACCTTGTGGCTAATGAATAC 1185
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A;Molecule type: protein
A;Residuss: 1-532 cOZO>
A;Cross-references: UNIPROT:P14943
A;Cross-references: UNIPROT:P14943
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase
C;Keywords: carboxylic ester hydrolase
E;32-517/Domain: cholinesterase homology <CHE>
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A34329
60K esterase (EC 3.1.1.-) isoform 2 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C;Accession: A34329
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A;Title: Isolation, properties, and the complete amino acid A;Reference number: A34329; MUID:89308686; PMID:2745458
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|ProAlaMetCysLeuGlnAsn---
CGGCACCGGCCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCT
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                                                                                                           ProLysHisLeumetAlaGlnPheGlnGlumetMetAlaAspAlaMetPheValMetPro
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                                                                                                                                           CTGACTGAAATCCGAGACAGTCTTCTGGACTTGCTTGGAGATGTGTTCTTTGTGGTCCCT
                                                                                                                                                                                                        CACATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAGCACTCC
                                                                                                                                                                                                                                        ArgGluIleMetHisGlnAlaThrLysGlnLeuMetLeu---------
                                                                                                                                                                                                                                                                                                     IleIleProLysLeuLeuAlaIleAspProGlnGluGluArgAspArgGlnAlaMet
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(C,Species: Homo sapiens (man)
(C,Species: Homo sapiens (man)
(C,Date: 10-Sep-199) #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
(C,Accession: JC5408
R,Schwer, H.; Langmann, T.; Daig, R.; Becker, A.; Aslanidis, C.; Schmitz, G.
Biochem. Biophys. Res. Commun. 233, 117-120, 1997
A;Title: Molecular cloning and characterization of a novel putative carboxylesterase, preparation of a novel putative carboxylesterase, preparation: JC5408
A;Reference number: JC5408; MUID:97289502; PMID:9144407
A;Accession: JC5408
A;Molecula type: manna
A;Residues: 1-559 <SCH>
A;Residues: 1-559 <SCH>
A;Residues: 1-559 <SCH>
A;Residues: UNIPROT:000748; GB:Y09616; NID:g2058317; PIDN:CAA70831.1; PID:g205831
A;Experimental source: intestine
C;Comment: This enzyme hydrolyzes many xenobiotics, such as carboxyl esters, thioesters &
                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: cholinesterase; cholinesterase homology C;Keywords: carboxylic ester hydrolase; glycoprotein F;58-544/Domain: cholinesterase homology c(HE> F;132-280,291-428/Disulfide bonds: #status predicted F;111,276/Binding site: carbohydrate (Asn) (covalent) #status F;228,457/Active site: Ser, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
JC5408
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C;Superfamily: chol
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                                 271
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                                                                                                                                                                                         26 GlyGlnAspSerAlaSerProIleArgThrThrHisThrGlyGlnValLeuGlySerLeu
                                                                                                                                                                                                                         GAGCAGTACCTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGG 1623
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                                                               ProProLeuGlyProLeuArgPheAlaProProGluProProGluSerTrpSerGlyVal
                                                                                                                          LeuGlnPheTrpThrHisThrLeuPro 516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AlaArgAsnArgAsnProAsnGlyGluGlyLeuAlaHisTrpProLeuPheAspLeuAsp 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTCGAACCGGGAATCCTAATGGGAACGACCTGTCTCTGTGGCCAGCTTATAATCTGACT 1563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspGluValValPheValPheArgSerHisLeuPheGlySerLysValProLeu-----
                                                                                            CCCCCCCTGCGATCTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDB:9959011
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1230.00
63.84%
46.70%
38.80%
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Matches:
Conservative:
Mismatches:
Indels:
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|||||||:::|||:::|||
|GluPheGlnHisGlnProSerTrpLeuLysAsnIleArgProProHisMetLysAlaAsp
                                              GTCCCTGCACTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTAT 1317
                                                                                          GlyAspProGlnThrLeuGlnAlaGlnPheGlnGluMetMetAlaAspSerMetPheVal
                                                                                                                                                                                                       GAGGCTCCTGAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAAAC 1137
                                                                                                                                                                                                                            GAGTTTCGGCACCGGCCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGAC
                                                                                                                ATCCTGCACATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAG
                                                                                                                                                                                   AspThrGlnLysGluMetAspArgGluAlaSerGlnAlaAlaLeuGlnLysMetLeuThr 377
                                                                                                                                                                                                                                                                          AAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACTCGAGTGGTTGATGGTGCT 969
                                                                                                                                                                                                                                                                                                                                                                  SerAlaCysAspGlnValAspSerGluAlaLeuValGlyCysLeuArgGlyLysSerLys 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-561 <SON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carboxylesterase (EC 3.1.1.1) precursor - golden hamster C;Species: Mesocricetus auratus (golden hamster) C;Date: 26-Dec-1994 #sequence_revision 03-Aug-1995 #text_change C;Date: 26-Dec-1996 #sequence_revision 03-Aug-1995 #text_change C;Accession: $47655 R;Sone, T.; Isobe, M.; Takabatake, E.; Wang, C.Y. Biochim. Biophys. Acta 1207, 138-142, 1994 A;Title: Cloning and sequence analysis of a hamster liver cDNA e: A;Reference number: $47655; MUID:94318665; PMID:8043605 A;Accession: $47655
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                                                                                                                                                                                                                                                                                                                              46 ValTyrValLysGluGlyValThrGlyValTyrAlaPheLeuGlyIleProPheAlaLys
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GTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCCTTTGCTGCT
                                                                               SerLysGluArgLysIleIleLeuProThrIleSerMetSerGluAspCysLeuTyrLeu
                                                                                                                         CAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTG
                                                                                                                                                              ArgAspGlyThrSerGluProAlaMetCysLeuGlnThrAspPheMetArgProGlnIle 105
                                                                                                                                                                                          CGAGAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTAGAT
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                                                                               CACGCTGATGAAGTCCGCTTTGTGTTTCGGTGGTGCCTTC-----CTGAAGGGGGACATT 143:
                                                                                                                                                            CGGCACCGGCCTCAGTGCTTT-----GAAGACACGAAGCCGGCTTTTGTCAAAGCCGAC
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carboxylesterase (EC 3.1.1.1) - mouse c.Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: S34607 R;Aida, K.; Moore, R.; Negishi, M. Biochim. Biophys. Acta 1174, 72-74, 1993 Biochim. Biophys. Acta 1174, 72-74, 1993 A;Reference number: S34607; MUID:93326638; PMID:7916639 A;Accession: S34607; MUID:93326638; PMID:7916639
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A;Molecule type: mRNA
A;Residues: 1-554 (ALD)
A;Croos-references: UNIPROT:Q63880; GB:S64130; NID:g404388; PIDN:AAB27606.1; PID:g404389
A;Croos-references: UNIPROT:Q63880; GB:S64130; NID:g404388; PIDN:AAB27606.1; PID:g404389
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase
F;46-536/Domain: cholinesterase homology <CHE>
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ATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCAGAAGACTGCCTCTACCTGAACATC
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LeuValHisAspAspGlnTyrLeuLysLeuAspIleGlnProAlaValGLyArgAlaLeu
                               GGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCCTATGAG
                                                                  TATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTGTGGTTCCCAGGA 456
                                                                                                                                   ThrieuAsnGluLysMetLysIlePheProIleSerGluAspCysLeuThrLeuAsnIle
                                                                                                                                                                                                     AlaSerIleAsnProProMetCysLeuGlnAspValGluArgMetSerAsnSerArgPhe
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                                                                                                          GCACTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTATGAGTTT 1323
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                           ACCTTTGCTCGAACCGGGAATCCTAATGGGAACGACCTGTCTCTGTGGCCAGCTTATAAT 1557
                                                         GATGAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTG-----AAGGGGGACATTGTTATG 1437
                                                                                                                                                                                                              ThrLeuIlePheSerLysTyrLeuGlnAppAlaGlyCysProValPheLeuTyrGluPhe
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carboxylesterase (EC 3.1.1.1) precursor - mouse (;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 09-Jul-2004 C;Accession: A39060 R;Ovnic, M.; Tepperman, K.; Medda, S.; Elliott, R.W.; Stephenson, D.A.; Grant, Genomics 9, 344-354, 1991 A;Title: Characterization of a murine cDNA encoding a member of the carboxylest A;Reference number: A39060; MUID:91189540; PMID:1840565 A;Accession: A39060 A,Status: preliminary A,Status: preliminary A,Status: preliminary
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Query Match:
DB:
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A; Residues: 1-554 < OVN>
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serProAlaAspLeuThrLysSerSerGlnLeuProValMetValTrpIleHisGlyGly
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                                                                                                                                      GAGGAGAAGTTACTGAGCCGGAAGATGATGAAAATACTGGGCTACCTTTGCTCGAACCGGG
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                                                                                          PheValPheGlyAlaProLeuLeuLys------GluGlyAlaSerGlu
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   GinIleGlyAlaThrThrGlnGlnAlaGlnArgLeuLysAlaGluGluValAlaPheTrp
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A;Molecule type: protein
A;Residues: 19-40 <MAT2>
A;Residues: 28-Lys and 33-Leu were also found
C;Superfamily: cholinesterase; cholinesterase homology
C;Ksyvords: carboxylic seter hydrolase; endoplasmic reticulum; glyc
F;11-18/Domain: signal sequence #status predicted <SIG>
F;11-18/Domain: signal sequence #status experimental <MAT>
F;19-56/Product: carboxylesterase #status experimental <MAT>
F;11-552/Domain: cholinesterase homology <CHE>
F;51-552/Domain: cholinesterase homology <CHE>
Townstading site: carbohydrate (Asm) (covalent) #status predicted
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Best Local Similarity:
Query Match:
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N;Alternate names: proline-beta-naphthylamidase
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C;Accession: S19307; S23607
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C;Accession: S19307; S23607
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A;Residues: 1-566 <MAT1>
A;Cross-references: UNIPROT:Q29550; EMBL:X63323; NID:g1930;
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                                                                                          GAAGACTGCCTCTACCTGAACATCTATGCGCCCTGCCCACGCCGATACAGGCTCCAAGCTC
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                                                                                                                                                                               GAGTGGCTGCTCTTAGATCAACACATGCTCAAGGTGCATTACCCGAAATTCGGAGTGTCA 372
                                                                                                                                                                                                                                             GAAGCCACCTACCCTAATTTGTGCCTCCAGAAC-----TCA
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ProValMetValTrpIleHisGlyGlyGlyGlyLeuValLeuGlyGlyAlaProMetTyrAsp
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GAGGAGAAGTTACTGAGCCGGAAGATGAATGAAATACTGGGCTACCTTTGCTCGAACCGGG
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                                                                                                                                                                                                                                                                                                                                                  GlnGluPheGlyTrpLeuLeuProThrMetMetGlyPheProLeuSerGluGlyLyBLeu 372
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                    GluGluValSerLeuSerLysThrValMetLysPheTrpAlaAsnPheAlaArgSerGly
                                                                   SerValPheGlyPheProLeuLeuLysGlyAsp-----
                                                                                         TTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAG
                                                                                                               SerPheSerSerAspLysLysProLysThrValIleGlyAspHisGlyAspGluIlePhe 472
                                                                                                                                      CAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGC 1395
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A;Experimental source: liver
(;Superfamily: Cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein; microsome
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-549/Product: carboxylesterase E1 #status predicted <MAT>
F;50-538/Domain: cholinesterase homology <CHE>
F;79,274,302,375,476/Binding site: carbohydrate (Asn) (covalent) #status
F;221,453/Active site: Ser, His #status predicted
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Best Local Similarity:
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A; Residues: 1-549 < TAK>
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TGGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCATCTTTGATGGGTCCGCCCTG
                                                                                                        TACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTCCCCGTCTTGGTG 444
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                                                                   TyrLeuAsnIleTyrSerProAlaAspLeuThrLysAsnSerArgLeuProValMetVal
                                                                                                                                                                    ThrGlyLysGluSerIleProLeuGluPhe--
                                                                                                                                                                                                                                                                                                            TACCCTAATTTGTGCCTCCAGAAC------
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                                                                                                                                             GluIlePheSerValPheGlyThrProPheLeuLys------GluGly
                                                                                                                                                                            GAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGACATTGTTATGTTCGAAGGA 1446
                                                                                                                                                                                                               TyrArgProSerPheValSerAspGlnArgProGlnThrValGlnGlyAspHisGlyAsp
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                                    TTCACCACATGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGACCAGGTGGCTGCT
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A;Note: differences between this sequence and other reports appear R;Kroetz, D.L.; McBride, O.W.; Gonzalez, F.J. Biochemistry 32, 11606-11617, 1993 A;Title: Glycosylation-dependent activity of baculovirus-expressed A;Reference number: A48809; MUID:94032283; PMID:8218228 A;Accession: I61085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 'G', 65-185, 'G', 187-361,363-567 < ZSC>
A; Cross-references: GB: X52973; NID: g36421; PIDN: CAA37147.1; PID
R; Riddles, P.W.; Richards, L.J.; Bowles, M.R.; Pond, S.M.
Gene 108, 289-292, 1991
A; Title: Cloning and analysis of a cDNA encoding a human liver
A; Reference number: PS0280; MUID: 92084150; PMID: 1748313
A; Accession: PS0280
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A;Cross-references: GB:M55509; NID:g179929; PIDN:AAA35650.1; PID:g179930
A;Cross-references: GB:M55509; NID:g179929; PIDN:AAA35650.1; PID:g179930
R;Shibata, F.; Takagi, Y.; Kitajima, M.; Kuroda, T.; Omura, T.
Genomics 17, 76-82, 1993
Genomics 17, 76-82, 1993
A;Title: Molecular cloning and characterization of a human carboxylesterase
A;Reference number: A47376, MUID:94010913; PMID:8406473
A;Accession: A47376
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A;Residues: 1-567 <MUNDA
A;Residues: 1-567 <MUNDA
A;Cross-references: UNIPROT:P23141; GB:M73499; NID:g179927; PIDN:AAA35
A;Note: parts of this sequence, including the amino end of the mature:
A;Long, R.M.; Calabrese, M.R.; Martin, B.M.; Pohl, L.R.
Life Sci. 48, PL43-PL49, 1991
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C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C;Accession: A41010; JH0327; Ā47376; A49816; PS0280; I61085; A48809; I57004
R;Munger, J.S.; Shi, G.P.; Mark, E.A.; Chin, D.T.; Gerard, C.; Chapman, H.A.
J. Biol. Chem. 266, 18832-18838, 1991
A;Tile: A serine esterase released by human alveolar macrophages is closely related A;Reference number: A41010; MUID:92011649; PMID:1918003
A;Accession: A41010
A;Molecule type: mRNA
A;Readdues: 1-55, 'G',57-361,363-535,'G',537-567 <KRO1>
A;Cross-references: GB:L07765; NID:g180949; PIDN:AAA35711.1; PID:g180950
A;Accession: A48809
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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A;Residues: 114,'H',116-280,'A',282-300,'IGNSYLWTYRETQREST',318-336,'R',338-382,'GSPI',38
A;Cross-references: GB:M65261; NID:g187028; PIDN:AAA83932.1; PID:g187029
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A;Residues: 1-17,'A',18-55,'G',57-535,'G',537-567 <KRO2>
A;Cross-references: GB:L07764; NID:g180947; PIDN:AAA16036.1; PID:g180948
C;Genetics:
A;Gene: GDB:CES1; HMSE
A;Cross-references: GDB:128044; OMIM:114835
A;Cross-references: GDB:128044; OMIM:114835
A,Map position: 16q13-16q22.1
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum; liver
F;1-18/Domain: signal sequence #status predicted <SIG>
F;1-19/Domain: bropeptide #status predicted <PRO>
F;50-553/Domain: cholinesterase homology <CHB>
F;146-567/Product: carboxylesterase Mstatus experimental <MAT>
F;564-567/Region: endoplasmic reticulum retention signal #status atypical
F;221,468/Active site: Ser, His #status predicted
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carboxylesterase (BC 3.1.1.1) ES-4 precursor, liver carboxylesterase (BC 3.1.1.1) ES-4 precursor, liver N,Alternate names: hydrolase B c,Species: Rattus norvegicus (Norway rat) C,Date: 28-Oct-1996 #sequence revision 13-Mar-1997 C,Accession: S62788; S51203; A55304; S49257 R;Robbi, M.; van Schaffingen, E.; Beaufay, H. Biochem. J. 313, 821-826, 1996
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R;Morgan, B.W.; Yan, B.; Greenway, D.; Petersen, D.R.; Parkinson, A. Arch. Blochem. Biophys. 315, 495-512, 1994
A;Title: Purification and characterization of two rat liver microsomal A;Reference number: S51202; MUID:95077430; PMID:7986098
A;Accession: S51203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Description: catalyzes conversion of carboxylic ester to alcohol and carboxylic C; Superfamily: cholinesterase; cholinesterase homology C; Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; liver F;1-18/Domain: signal sequence #status predicted <SIG>F;19-561/Product: carboxylesterase ES-4 #status experimental <MAT>
T;19-561/Product: carboxylesterase ES-4 #status experimental <MAT>
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J. Biol. Chem. 269, 29688-29696, 1994
A;Title: Rat kidney carboxylesterase. Cloning, sequencing, cellular localization,
A;Reference number: A55304; MUID:95050819; PMID:7961958
A;Accession: A55304
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A; Residues: 1-561 < RO2>
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A; Residues: 1-6, 'F', 8-59, 'P', 61-212, 'A', 214-252, 'T', 254-309, 'IT', 312-341, 'N', 343-424, 'FY
A; Cross-references: GB: U10697; NID: g562007
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A; Residues: 1-561 < ROB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;50-551/Domain: cholinesterase homology <CHE>;221,466/Active site: Ser, His #status predicted;301/Binding site: carbohydrate (Asn) (covalent) #status
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GACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTTCGGT 1407
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                                                              ArgAspAlaGlyAlaProThrTyrMetTyrGluTyrGlnTyrTyrProSerPheSerSer 455
                                                                                                   AGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTGCTTTGAA
                                                                                                                                           LeuAlaPheIleGlyAspValSerPheSerIleProSerValMetValSerArgAspHis
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A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-562 cOVN-
A;Residues: 1-562 cOVN-
A;Cross-references: UNIPROT:Q64176; GB:S80191; NID:g244727; PIDN:AAB21335.1; PID:g244728
A;Cross-reference extracted from NCBI backbone (NCBIN:80191, NCBIP:80194)
C;Superfamily: cholinesterase; cholinesterase homology
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum
F;51-552/Domain: cholinesterase homology <CHE>
F;222,467/Active site: Ser, His #status predicted
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C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C;Accession: A55281
R;Ovnic, M.; Swank, R.T.; Fletcher, C.; Zhen, L.; Novak, E.K.; Baumann, H.; He Genomics 11, 956-967, 1991
A;Title: Characterization and functional expression of a cDNA encoding egasyn A;Reference number: A55281; MUID:92147141; PMID:1783403
A;Accession: A55281; MUID:92147141; PMID:1783403
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N;Alternate names: beta-glucuronidase endoplasmic reticulum-targeting protein;
C;Species: Mus musculus (house mouse)
C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
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                 AlaProIleLeuArgGly---
                                            GGTGCCTTCCTGAAGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGAGAAGTTA 1467
                                                                                                      GACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTTCGGT
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A; ROBICULE: 1740 CLONS
A; Residues: 1-540 CLONS
A; Crobs-references: UNIPROT: P10959; GB: M20629; GB: X13587; NID: g203279; l2; Crobs-references: UNIPROT: P10959; GB: M20629; GB: X13587; NID: g203279; l2; Crops-references: UNIPROT: P10959; GB: M20629; GB: X13587; NID: g203279; l2; Crops-references: Growth of the state production of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state product of the state 
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R;Long, R.M.; Satch, H.; Martin, B.M.; Kimura, S.; Gonzalez, F.J.; Pohl, L.R. Biochem. Biophys. Res. Commun. 156, 866-873, 1988
A;Title: Rat liver carboxylesterase: cDNA cloning, sequencing, and evidence for A;Reference number: A31584; MUID:89050119; PMID:2973315
A;Accession: A31584
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A31584
A31584
Carboxylesterase (BC 3.1.1.1) precursor - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-May-1990 #sequence_revision 03-Aug-1992 #text_change 09-Jul-2004
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TyrProProMetCysSerGlnAspGlyValValGlyLysLeuLeuAlaAspMetLeuSer
                                                                                                                                                                                                                           TACCCTAATTTGTGCCTCCAGAAC-----TCAGAGTGGCTGCTC
                                                                                                                                                                                                                                                            CTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTGCGAGAAGCCACCTCC
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                                                                                                             ThrGlyLysGluSerIleProLeuGluPhe-----SerGluAspCysLeu
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                                    TyrLeuAsnIleTyrSerProAlaAspLeuThrLysAsnSerArgLeuProValMetVal
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                                                                                                                                GluIlePheServalPheGlyThrProPheLeuLy8------GluGly
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A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-561 <YAN>
A;Residues: 1-561 <YAN>
A;Residues: 1-561 <YAN>
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C;Function:
A;Bescription: catalyzes conversion of carboxylic ester to alcohol and carboxylic a;Description: catalyzes conversion of carboxylic ester to alcohol and carboxylic C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; liver
F;1-18/Domain: signal sequence #status predicted <SIG>
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Arch. Biochem. Biophys. 317, 222-234, 1995
A;Title: Cloning and expression of hydrolase C, a member A;Reference number: S71597; MUID:95177656; PMID:7872788
A;Accession: S71597
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;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998
C;Accession: S71597
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S71597
Carboxylesterase (EC 3.1.1.1) precursor, liver -
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AlaSerLeuGluGlyValThrGlnSerValAlaValPheLeuGlyValProPheAlaLys
 GTCTTGGTGTGGGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGG
                                             AspCysLeuTyrLeuAsnIleTyrThrProAlaAspPheThrLysAspSerArgMetPro
                                                                  GACTGCCTCTACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCCAAGCTCCCC
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GAGGAGAAGTTACTGAGCCGGAAGATGATGAAAATACTGGGCTACCTTTGCTCGAACCGGG
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Qy 217 CTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCTGGGATAACTTGCGAGAA 276	Qy 157 GTGCTGGGAAGCCCTGTGAACGTGTTCCTCGGAGTCCCCCTTTGCTGCTGCTCCCCCG 216 :::	Qy 97 TCTGCTGAAGGGCCACAGAGGAACACCAGGCTGGGATTGAATTCAGGGCAAGCAA	37 TGCTTTTTCCTGATTCTCCA ::: :::::: 2 CysLeuTyrAlaLeuIleLe	Ouery Match: 35.43% Indels: 56 DB: 2 Gaps: 11 US-10-023-515-3 (1-1746) x JC2447 (1-561)	nment Scores: . No.: 8.04e-79 B: 1123.00 Matches: 1123.07 Conservative:	F;79,107,489/Binding site: carbohydrate (Asn) (covalent) #status predicted F;221,466/Active site: Ser, His #status predicted	c ester hydrolase; c ester hydrolase; c ester hydrolase; c c c c c c c c c c c c c c c c c c c	A; Molecule type: mRNA A; Residues: 503-554, 'R', 556-561 <med> A; Residues: 503-554, 'R', 556-561 <med> A; Cross-references: EMBL: X65295, NID: g57557; PIDN: CAA46390.1; PID: g57558 A; Cross-references: EMBL: X65295, Chlingtererse homology</med></med>	801-806, 1992 8terase family es 3460; MUID:922990	NIPROT:Q63108 NIPROT:Q63108	A;Reference number: JC2447; MUID:95032008; PMID:7945287 A;Recession: JC2447 A;Accession: JC2447 A;Accession: JC2447 A;Accession: JC2447 A;Accession: JC2447	47; S23462 fay, H. Res. Commun. 203, 1404-1411, 1994	C:Date: 29.Mar-1006 #segmence revision 26-May-1995 #text Change 09-701-2004 C:Date: 29.Mar-1906 #segmence revision 26-May-1995 #text Change 09-701-2004	546 ThrGlnLeuLeu	::: 	OY 1516 AATCCTAATGGGAACGACCTGTCTCTGTGGCCAGCTTATAATCTGACCAGTACCTC 1575	
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A;Mclecule type: mRNA
A;Residues: 1-264, 'K', 266-565 <a href="ROB2">A;Cross-references: EMBL:X51974; NID:956898; PIDN:CAA36236.1; PID:956899">A;Cross-references: EMBL:X51974; NID:956898; PIDN:CAA36236.1; PID:956899
R;Morgan, E.W.; Yan, B.; Greenway, D.; Petersen, D.R.; Parkinson, A.
Arch. Blochem. Biophys. 315, 495-512, 1994
A;Title: Purification and characterization of two rat liver microsomal carbox A;Reference number: S51202; MUID:95077430; PMID:7986098
A;Accession: S51202
A;Molecule type: protein
A;Residues: 19-48 <a href="MOR">MOR</a>>
A;Title: The carboxylesterase family exhibits C-terminal sequence diversity r
A;Accession: S23460; MUID:92299008; PMID:1606962
A;Accession: S23460; MUID:92299008; PMID:1606962
A;Status: preliminary; translation not shown
A;Residues: 1-185,'Q',187-422,'M',424-505,'N',507-565 <a href="MOECULE type: mRNA">MOECULE type: mRNA</a>
A;Residues: 1-185,'Q',187-422,'M',424-505,'N',507-565 <a href="MOECULE type: mRNA">MOECULE type: mRNA</a>
A;Gaustad, R.; Sletten, K.; Lovhaug, D.; Fonnum, F.
Biochem. J. 274, 693-697, 1991
A;Title: Purification and characterization of carboxylesterases from rat lung A;Reference number: S14361; MUID:91190080; PMID:2012599
A;Residues: 19-26,'D',28-37 <GAU>
C;Superfamily: chollnesterase; chollnesterase homology
C;Superfamily: chollnesterase; chollnesterase homology
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A;Molecule type: mRNA
A;Residues: 1-565 <ROB1>
A;Cross-references: UNIPROT:Q9R135; EMBL:X51974
A;Note: 168-Gln, 247-Lys, 423-Met, and 506-Asn were also found
A;Note: the sequence from Fig. 4 is inconsistent with that from R;Robbi, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N;Alternate names: hydrolase A
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change
C;Accession: S10367; S12468; S51202; S23460; S14361
R;Robbi, M.; Beaufay, H.; Octave, J.N.
Biochem. J. 269, 451-458, 1990
A;Title: Nucleotide sequence of cDNA coding for rat liver pI 6.1
A;Reference number: S10367; MUID:90351366; PMID:2386485
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C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; homotrimer F;1-18/Domain: signal sequence #status predicted <SIG> F;19-565/Product: carboxylesterase #status predicted <MAT> F;50-551/Domain: cholinesterase homology <CHE> F;79,489/Binding site: carbohydrate (Asn) (covalent) #status predicted F;221,466/Active site: Ser, His #status predicted
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AlaLeuIleThrThrAspSerLysProIleAlaAsnLeu-----IleAlaThrLeuSer
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-UNITS_bite -START=1 =RND=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR SCORE=pot -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=664091 @CGN 1 1 389 @runat 14062005 133459 9335 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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ALIGNMENTS

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MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Bichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Balakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,

Janes S. T. Marra M.A.
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FLJ31547 protein.
Name=FLJ31547;
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                                                                                              Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 and mouse cDNA sequences.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  SEQUENCE FROM N.A.
TISSUE=PCR rescued clones;
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-- SIMILARITY: Belongs to the type-B carboxylesterase/lipase EMBL; BC069501; AAH69501.1; -- HSSP; P12337; IX4Y.

G0; G0:0003824; F:catalytic activity; IEA.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR00379; Ser_estrs.
Pfam; PF00135; CC0esterase; 1.
PROSITE; PS00142; CARBOXYLESTERASE_B_1; 1.
PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
Hydrolase.

SEQUENCE 575 AA; 63926 MW; 6F5B735BDEFC9C09 CRC64;
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RX PubMed=1470209; DOI=10.1038/ngl285;
RX PubMed=1470209; DOI=10.1038/ngl285;
RA Ota T., Suzuki Y., Niehikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Niehi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.;
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka M., Yamazaki M.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Pujii A., Hara H., Tanase T., Kusano J.,
RA Togiya S., Momiyama H., Satoh N., Takami K., Antuka S.,
Yoshikawa Y., Mateunawa H., Ichhara T., Shiohata N., Sano S.,
RA Yoshikawa Y., Mateunabe H., Satoh N., Takami S., Takuzumi Y.,
RA Yamazaki M., Watanabe K., Kunagai A., Itakura S., Fukuzumi Y.,
RA Hishigaki H., Watanabe K., Kunagai A., Itakura S., Fukuzumi Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Matanata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Senba T.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Kawabata A., Hakamura Y., Ohara O., Isogai T., Sugano S.;
RA Okumura K., Mada T., Makamura Y., Ohara O., Isogai T., Sugano S.;
RA RA Genet. 36:40-45(2004).
RB ROIPENCE PROM N.
                                                                                                                                                                                                              MEDLINE=2238257; Pubmed=1,477932; DOI=10.1073/pnas.242603899;

AS Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

AK Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

AA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

AA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

AA Hopkins R.F., Jordan H., Moore T., AA., Rubin G.M., Hong L.,

AA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

AA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

AB Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

AA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

AA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

AA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

AA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

AN Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

AN Hilling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

AA Whiting M., Madan A., Young A.C., Shevchenko Y., Butterfield Y.S.,

AN Mores S. T. May A., Schmutz J., Myers R.M., Schein J.E.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                  TISSUE=PCR rescued clones;
Strausberg R.;
                                                                                                                                                              Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 and mouse cDNA sequences.";
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SIMILARITY: Belongs to the type-B
L; AK056109; BAB71094.1; -.
L; BC069548; AAH69548.1; -.
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                                                   (APR-2004) to the EMBL/GenBank/DDBJ databases
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InterPro; IPR000379; Ser_estrs.
Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.
PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.
Hydrolase; Hypothetical protein.
SEQUENCE 525 AA; 58200 MW; 7724878B8A22F215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO: 0016787; F:hydrolase activity; IBA.
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                                  SerAlaGlyAlaIleSerValSerSerLeuIleLeuSerProMetAlaLysGlyLeuPhe
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                                                                                                                                                                                                  GTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGCGAG
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Matches:
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Hypothetical protein FLJ33678.
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RX PubMed=14702039; DOI=10.1038/ng1285;
RA Gra T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Minomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Moriya S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
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RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Yamashita R.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Yamashita R.,
RA Nishashi R., Kawama R., Takami O., Isogai T., Sugano S.;
RA Nakai K., Walama M., Takama O., Ohmoti Y., Makagawa K.,
RA Makai
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"cauxin family protein.";

Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.

L. Submitted (AUG-2004) to the type-B carboxylesterase/lipa

REMBL, AB186392; BAD35015.1; -.

RGO; GO:0003824; F:catalytic activity; IEA.

RINterPro; IPR002018; CarbesteraseB.

InterPro; IPR000379; Ser_estrs.

R pfam; PF00135; COesterase; 1.

R PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.

R PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.

W Hydrolase.

9 SEQUENCE 575 AA; 63620 MM; 1005C35E82E1183D CRC64;
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Q6AW47;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
MCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Carboxylesterase-like urinary excreted protein.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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US-10-023-515-3 (1-1746) x Q6AW46 (1-575)
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"cauxin family protein.";

"cauxin family protein.";

Submitted (AUG-2004) to the EMBL/GenBank/DDBJ dat

-i SIMILARITY: Belongs to the type-B carboxylest

EMBL; AB186393; BAD35016.1; -.

GO; GO:0003824; F:catalytic activity; IEA.

InterPro; IPR002018; CarbesteraseB.

InterPro; IPR002079; Ser_estrs.

PROSITE; PS00135; COesterase; 1.

PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.

PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.

Hydrolase.

SEQUENCE 575 AA; 64166 MW; 3EB9D85981D9DE0A C
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Carboxylesterase-like urinary excreted protein.
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TISSUE=Kidney;

MEDLINE=22458314; PubMed=12401131; DOI=10.1042/BJ20021446;

Miyazaki M., Kamiie K., Soeta S., Taira H., Yama8hita T.;

Miyazaki M., Kamiie K., Soeta S., Taira H., Yama8hita T.;

Molecular cloning and characterization of a novel carboxylesterase-
like protein that is physiologically present at high concentrations in
the urine of domestic cats (Felis catus).";

Biochem. J. 370:101-110(2003).

1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.

EMBL; AB045377; BAC22577.1; -.

GO; GO:0016787; F:hydrolase activity; IEA.

GO:0016787; F:hydrolase activity; IEA.
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InterPro; IPR000379; Ser_estrs.
Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE_B_1;
PROSITE; PS00941; CARBOXYLESTERASE_B_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q81034 PRELIMINARY; PRT; 545 AA.
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Carboxylesterase-like urinary excreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00122;
PROSITE; PS00941;
Hydrolase.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                             Hypothetical protein.

Hypothetical protein.

Hypothetical protein.

Hypothetical protein.

Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Bukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euceleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Macaca.
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О.:
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ATCATCCCTTACCTGGAGGCCCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCA
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SerValSerValGlyGlnLysLeuLysGluGlnGluValGluPheTrpMetAsnThrIle
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GluGlyValProLeuTypProAlaTyrThrGlnSerGluGlnTyrLeuLysLeuAspLeu
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1676.50
96.47%
95.00%
52.89%
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Matches:
Conservative:
Mismatches:
Indels:
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01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation updat
                                Anas platyrhynchos (Domestic duck).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo:
Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas
                                                            Fatty acyl-CoA hydrolase precursor, (Thioesterase B).
                                                                                                                  SASB ANAPL
SEQUENCE FROM N.A., AND TISSUB-Uropygial gland;
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"Molecular cloning and sequencing of thioesterase B gene associated wit stimulation of expression of the thioesterase B gene associated wit hormonal induction of peroxisome proliferation.";

J. Biol. Chem. 268:14278-14284(1993).

-I-FUNCTION: Fatty acid biosynthesis chain termination and release the free fatty acid product is achieved by hydrolysis of the the seter by a thioesterase. This thioesterase may be associated wit peroxisome proliferation and may play a role in the production alphydroxy fatty acid diester pheromones.

-I-TISSUE SPECIFICITY: Highest levels in uropygial gland, much low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A47162; A47162.

HSSP; O77540; IKAY.

InterPro; IPRO02018; CarbesteraseB.

InterPro; IPR000379; Ser_estrs.

Pfam; PF00135; COesterase; 1.

PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.

PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.

PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                              liver and kidney.
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GAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAGCTC
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GlyGlnTyrLeuSerAspAlaIleThrAsnArgLysGluLysValArgLeuGlnIleSer
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ValArgAspAlaAlaSerTyrProProMetCysLeuGlnAspLys--
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Acyl-ester intermediate (By similarity).
Charge relay system (By similarity).
Charge relay system (By similarity).
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N-linked (GlcNAc. . .) (Potential).
; 03E35D90A037F6B0 CRC64;
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PheProGluPheThrGluGlyLeuGluLysAspValAlaArgGlnValLeuGlnSerThr 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaGluMetGluGlnIleThrLeuLysMetProProMetPheIleSerAlaSerLeuAsp
                                                                 VallysAlaAspHisAlaAspGluIleAlaPheValPheGlyLysProPheLeuAlaGly
                                                                                                  GTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGG
                                                                                                                                                                                                      ProLeuPheValPheSerAlaValGluValAlaArgHisHisArgAspAlaGlyAsnPro
                                                                                                                                                                                                                                                                                                                                         LeuAlaLeuSerPheLysGlyAlaProSerAspIleValAspLeuValTyrAsnGluTyr 395
                                                                                                                                                                                                                                                                                                                                                                          CTGCACATC------CCGCCTCAGTATTTGCACCTTGTGGCTAATGAATAC 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProTyrIleIleGlyValAsnAsnCysGluPheGlyTrpIleLeuProArgMetMetLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTTCCATCATCGGAGTCAATAACCACGAGTGTGGCTTCCTGCTGCCT---ATGAAGGAG 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GiyValPhePheProLysSerProArgGlnLeuLeuSerGluLysValIleAsnAlaVal 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGAGCTG-----CTGACCCTCAGCCAGAAAACAAAGTCTTTCACTCGAGTGGTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AlaGiyCysGluLysSerSerSerAlaAlaLeuValGluCysLeuArgGluLysThrGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuPheThrGlu------GlnProGluGluGlnAlaGlnArgIleAlaAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTGTGACCATCTTTGGCGAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGGTGGCTGCTCTGTCCTGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IleAlaGlyTyrPheSerThrGlyAspLysHisAlaArgGlyAsnTrpGlyTyrLeuAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCATGGCCAAAGGCTTATTCCACAAAGCCATCATGGAGAGTGGGGGTGGCCATC---ATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATATTTGGTTTCTTCACCACATGGGATCAGCATGCTCCGGGGAACTGGGCCTTCAAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlySerAlaLeuAlaAlaPheAspAsnValValValThrIleGinTyrArgLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluAspCysLeuTyrLeuAsnValTyrThrProValSerThrGluGluGlnGluLysLeu 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGTCCGCCCTGGCTATGAGGACGTGCTGGTTGTGGTCGTCCAGTACCGGCTAGGA
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RC STRAIN=FVB/N; TISSUE-Colon, and Kidney;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiteh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Guellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Brownstein M.J., Ugdin T.B., Toshyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Robask S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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(991WG0;
(901WG0;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 28, Last sequence update)
01-DEC-2004 (TrEMBLrel. 28, Last annotation update)
Carboxylesterase 2 (Carboxylesterase ML3 precursor).
Name=Ces2; Synonyms=ces2A3;
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmanalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                   Strausberg R.;
Submitted (JUN-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Kidney;
                                SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon,
                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                          Strausberg
Submitted
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1546
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ArgArgArgLysHisThrAspLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (OCT-2001)
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                                and Kidney;
                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases
                                                                                                                                EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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PROSITE; PS00941; CARBOXYLESTERASE B_2;
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                                                       STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
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Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
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Genome Res. 10:1757-1771(2000).
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STRAIN-C57BL/6J; TISSUE-Cvary and uterus;

MEDLINE-20499374; PubMed=11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new ge-
genome Res. 10:1617-1630(2000).
   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II was I in the mouse transcriptome based on functional 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Ovary and uterus; MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
05-JUL-2004 (TrEMBLrel. 23, Last sequence update)
05-JUL-2004 (TrEMBLrel. 23, Last sequence update)
Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
RIKEN full-length enriched library, clone:5031415B19 product:similar
to CARBOXYLESTERASE (EC 3.1.1.1) (ALI-ESTERASE) (B-ESTERASE)
(MONOBUTYRASE) (COCAINE ESTERASE) (PROCAINE ESTERASE) (METHYLBUTYRASE)
(9030624L02R1k protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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01-MAR-2003
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DB:
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RM MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Altschul S.F., Jordan H., Moore T., Robin G.M., Hong L.,

RA Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Blatchenko L., Washina K., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Blatchenko L., Washina K., Farmer A.A., Rubin G.M., Hong L.,

RA Blatchenko L., Washina R., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Blatchenko L., Washina R., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Blatchenko L., Washina R., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Blatchenko L., Washina R., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Blatchenko L., Matan D., M., Scheman M.J., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blatchely R.W., Tuchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

A Tones S. T. Marra M.A.,

RA Rodriguez R.M., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Tones S. T. Marra M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (JUL-2003) to the EMBL
-!- SIMILARITY: Belongs to the t:
EMBL; AK077248; BAC36707.1; -.
EMBL; BC055062; AAH55062.1; -.
HSSP; P12337; 1K4Y.
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Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hayashida K., Hayatsu N., Eshii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Mateuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:2443170; 9030624L02Rik.
GO; GO:0005615; C:extracellular space; 7
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser estre.
Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE B 1;
PROSITE; PS00941; CARBOXYLESTERASE B 2;
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STRAIN=FVB/N; TISSUE=Colon;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Generation and initial analysis of more than 15,000 and mouse cDNA sequences.";
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                                                              151 GTCACTGTGCTGGGAAGCCCTGTGCCTGTGAACGTGTTCCTCGGAGTCCCCTTTGCTGCT
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GlyGlnAspSerAlaSerProIleArgAsnThrHisThrGlyGlnValArgGlySerLeu
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TISSUE=Colon;
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63.48%
48.69%
40.41%
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the type-B carboxylesterase/lipase family.
                                                                                                                                                                                                                                                                      (1-559)
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Matches:
Conservative:
Mismatches:
Indels:
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|----ThrArgLysThrLeuProAlaValLeu
                                                                                                                                                     ||| |||::::::||||||
AspGluTyrGlyTrpIleLeuProThrIleMetAspProAlaGlnLysIleGluGluIle
                                                                                                                                                                                                                                                                                                                                        GACTCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAACCCTCCAAGGAGCTGCTGACCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                 GGCGAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGC
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                                                                                                                                                                                CACGAGTGTGGCTTCCTGCTGCCT-----
                                                                                                                                                                                                                                                       ::::::
AsnLysValPheLysIleIleProGlyValValAspGlyGluPheLeuProLysHisPro
                                                                                                                                                                                                                                                                                                           :::|||||| ||| :::||| :::
AsnSerGluThrLeuMetCysCysLeuArgGlyLysAsnGluAlaGluMetLeuAlaIle
                                                                                                                                                                                                                                                                                                                                                               SerSerGluMetValHis-----ArgIleValAlaAsnLeuSerGlyCysAlaAlaVal
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                        AspLeuLysMetMetAsnLeuIleLeuProProIleSerMetSerGluAspCysLeuTyr
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                                                                          ATACAAAACATCCTGCACATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTC
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                                                 -LeuProProGluCysGlyAspLeuLeuMetGluGluTyrMet
                                                                                                   -LysSerThrAlaLeuLysMet
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                                                                                                                                                                                                  PE SEQUENCE FROM N.A.

(C STRAIN=Syrian golden; TISSUE=Liver;
(C STRAIN=Syrian golden; TISSUE=Liver;
(C SONE T., Ishida Y., Takabatake E., Wang C., Isobe M.;
(A Sone T., Ishida Y., Takabatake E., Wang C., Isobe M.;
(A Sone T., Ishida Y., Takabatake E., Wang C., Isobe M.;
(C -|- SIMILARITY: Belongs to the type-B carboxylesterase/lipase fam.)
(C -|- SIMILARITY: Belongs to the type-B carboxylesterase/lipase fam.)
(C -|- SIMILARITY: Belongs to the type-B carboxylesterase activity; IEA.
(R EMBL; D50577; BAA23605.1; -.
(R GO; GO:0016787; F:hadrolase activity; IEA.
(R GO; GO:0016787; F:hydrolase activity; IEA.
(R GO; GO:0016787; F:hydrolase activity; IEA.
(R InterPro; IPR0002018; CarboxylesteraseB.
(R InterPro; IPR000386; ER_target_S.
(R InterPro; IPR000399; Ser_estrs.
(R PROSITE; PS00141; CARBOXYLESTERASE B 1; 1.
(R PROSITE; PS00141; CARBOXYLESTERASE B 2; 1.
(R PROSITE; PS00014; ER_TARGET; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 05, Last annotation updat
Carboxylesterase precursor (EC 3.1.1.1)
Mesocricetus auratus (Golden hamster)
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                                                                                                                                                        Hydrolase; Signal.
SIGNAL 1
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Sone T., Wang C.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Microsomal amidases and carboxylesterases.";
(In) Guengerich F.P. (eds.);
COMPREHENSIVE TOXICOLOGY VOLUME 3, Biotransformation, pp.265-281,
Pergamon, Oxford (1997).
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male colon cDNA, RIESN full-length enriched
library, clone:9030624L02 product:similar to CARBOXYLESTERASE;
3.1.1.1 (ALI-ESTERASE) (B-ESTERASE) (MONOBUTYRASE) (COCAINE ESTERASE)
(PROCAINE ESTERASE) (METHYLBUTYRASE).
                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Colon;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSORTIUM;
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STRAIN=C57BL/60; TISSUE=Colon;

MEDLINE=99279253; PubMed=10349636;

Carninci P. Hayashizaki Y.;

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"Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                     DOI=10.1016/S0076-6879(99)03004-9;
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RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Mateuyama T., Miyazaki A., Murata M., Koya S.,
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RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
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C. -- SIMILARITY Belongs to the type-B carboxylesterase/lipase family.
REMBL; AK033563; BAC28361.1; --
REMBL; AK0337; IKAY.
                                                                                       US-10-023-515-3 (1-1746) x Q8BM97 (1-559)
                                                                                                                                                    Percent Similarity:
Best Local Similarity:
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
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STRAIN=C57BL/6J; TISSUE=Colon;

MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new 'ge

Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                     InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs.
Pfam; PP00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE B_1;
PROSITE; PS00941; CARBOXYLESTERASE_B_2;
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MGD; MGI:2443170; 9030624L02Rik.
GO; GO:0005615; C:extracellular space;
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RP SEQUENCE FROM N.A.

RC STRAIN=YPW/N; TISSUE-Colon;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMed=12.

RA Altasner R.D., Collins F.S., Wagner L., Schuler G.D.,

RA Altasner R.D., Collins F.S., Wang J., Heine F.,

RA Altasner R.D., Collins F.S., Ramer A.A., Rubin G.M., Hong L.,

RA Hopkins R.P., Joaches M.B., Bonaldo M.F., Casavant T.L., Scheetz T.S.,

RA Stapleton M., Suddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Robesk S.A., WcEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Robesy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Alones S.J., Marra M.A.;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence up
05-JUL-2004 (TrEMBLrel. 27, Last annotation
Hypothetical protein BC015286.
Name=BC015286.
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                       Strausberg R.;
Submitted (SEP-2003) to
                                                                   SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                           Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                    mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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InterPro; IPR000379; Ser_estrs.
Pfam; PF00135; COseterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE B_1;
PROSITE; PS00941; CARBOXYLESTERASE B_2;
Hydrolase; Hypothetical protein.
SEQUENCE 556 AA; 61927 MW; 58DE05A3;
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HSSP; P12337; 1K4Y.
G0; G0:0016787; F.hydrolase activity;
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                                                TCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTATTCCACAAAGCCATCATGGAGAGT
                                                                                                                               TTCGGTGGGGACCCCAGCTCTGTGACCATCTTTGGCGAGTCCGCGGGAGCCATAAGTGTT
                                                                                                                                                                                                GTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACCACATGGGATCAGCATGCTCCGGGG
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05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, LOC443703 protein (Fragment) Name=LOC443703;
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|GlyValAlaLeuLeuProTyrLeuIleThrAspThrSerGluMetValSer-----Thr
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AsnLeuGlnAlaValLeuLysAsnThrThrAlaGlnLeuMetLeuProProGluCysSer
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RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Hothring M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Saalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
RT and mouse cDNA sequences.",
RT and mouse cDNA sequences.",
RT and mouse cDNA sequences.",
RT and mouse cDNA sequences.",
                                                                                                                                                                                                                                                                                                                                                                Klein S., Gerhard D.S.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
-!-SIMILARITY: Belongs to the type-B carboxylesterase/lipase EMBL; BC074230; AAH74230.1; -.
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR0002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs.
Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.
PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.
                                                                                                                                                                                                                      Local Similarity:
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MEDLINE-22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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TISSUE=Kidney;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                          ATCCCGCCTCAGTATTTGCAC--------CTTGTGGCTAATGAATAC 1185
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                                                                                                                                                                                                                                                                                                                         Sone T., Kunitomo T., Isobe M.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: Belongs to the type-B carboxylesterase/lipase
EMBL; AB010632; BAA25691.1; -.
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                                                                                                                                                                                                                                                              HSSP; P37967; 1QE3.
GO; GO:0004091; F:carboxylesterase activity;
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs.
                                                                                                                                                                                                                      Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE_B_1;
PROSITE; PS00941; CARBOXYLESTERASE_B_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Carboxylesterase precursor (EC 3.1.1.1)
                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Wistar; TISSUE=Small intestine, Sone T., Kunitomo T., Isobe M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                           Hydrolase; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
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MetIleProAlaValValAspGlyGluPheLeuProArgHisProLysGluLeuLeuAla
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ThrValSerThrThrValAlaLysLeuSerGlyCysGluAlaMetAspSerGluAlaLeu
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                                                                                                                                          CTGAGGTGCCTGAGGACAAAACCCCTCCAAGGAGCTGCTGACCCTCAGCCAGAAAACAAAG
                                                                                                                                                                                                                                                                   ATGGAGAGTGGGGTGGCCATCATCCCTTACCTGGAGGCCCCATGATTATGAGAAGAGTGAG
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                                                                               TGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTT 1398
                                                                                                                                                                                                                                    AGCACCATCCCC 1650
                                   CTGGACTTGAACATGAGCCTCGGACAGAGAGCTCAAAGAACCGCGGGTGGATTTTTTGGACC 1638
                                                                                                          GTGTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAG 1458
                                                                                                                                                                                                                        CysGlyAspLeuLeuMetGluGluTyrMetGlyAsnThrAspAspSerGlnThrLeuGln 406
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                        LeuAspThrHisProAlaValAspArgAlaLeuLysAlaArgArgLeuGlnPheTrpThr 541
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Search completed: June 15, 2005, 08:53:13
Job time: 183.861 secs



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Result
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-MODEL-frame+ n2p.model -DEV=xlh
-Op-/cgn2 1/USPTO spool/6664091/runat_14062005_133500_9360/app_query.fasta_1.4238
-DB-Issued_Patents_AA -QFMT=fastan -SUFFIX=n2p.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -WATRIX=blosum62 -TRANS=human40.cdi
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-LOOPEXT=0 -UNITS=bits -START=1 -END==10 -THR_MIN=0 -ALIGN=15
-MODES-LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=664091 @CGN_1 1 54 @runat_16205_133500_9360 -NCPU=6 -ICPU=3 -NO_MMAP
-LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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US-09-146-661-2

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                                                APPLICANT: Danks, Mary K.
APPLICANT: Potter, Philip M.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Method
TITLE OF INVENTION: Tumor Cells
FILE REFERENCE: SJ-005
CURRENT APPLICATION NUMBER: US/9/595,682B
CURRENT FILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: 60/075,258
PRIOR FILING DATE: 1998-02-19
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR PILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 559
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                           Sequence 6426, Application US/09949016 Patent No. 6812339
                                                                                         ORGANISM: Human
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                                            ATCATCGGAGTCAATAACCACGAGTGTGGCTTCCTGCTGCCT-----ATGAAG 1071
                                                                  ||| ||| ||| ::: |||||||::: ||||||||| PheLeuProArgHisProGlnGluLeuLeuAlaSerAlaAspPheGlnProValProSer 337
                                                                                          AAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACTCGAGTGGTTGATGGTGCT 969
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Percent Similarity:
Best Local Similarity:
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241.755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGCGGGTGGATTTTTTGGACCAGCACCATCCCC 1650
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APPLICANT: Potter, Philip M.
APPLICANT: Potter, Philip M.
APPLICANT: Houghton, Peter J.
TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: Tumor Cells
TITLE REPERENCE: SJ-005
CURRENT APPLICATION NUMBER: US/09/595,682B
CURRENT FILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: 60/075,258
PRIOR PILING DATE: 1998-02-19
PRIOR PILING DATE: 1998-02-12
PRIOR PILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
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                                                         US-10-023-515-3 (1-1746) x US-09-595-682B-21 (1-565)
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                                                                                                                                                                                                                                                                                                                               SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   LENGTH: 565
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
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|LeuProValMetValTrpIleHisGlyGlyGlyLeuMetValGlyGlyAlaSerThrTyr 152
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                                                                             GlyAspProLysGluAsnThrAlaPheLeuThrThrVallleAspGlyValLeuLeuPro 328
                                                                                                                                                         ThrGluGluGluLeuMetGluValThrLeuLysMetLysPheMetAlaLeuAspLeuVal 308
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Engineering Plant Resistance to Pyridines TITLE OF INVENTION: Expression of Esterase Enzymes FILE REFERENCE: 38-21 (10551) RLB3 Pyridine Tolerance CURRENT APPLICATION NUMBER: US/09/264,737A CURRENT FILING DATE: 1999-03-09 EARLIER APPLICATION NUMBER: 60/077,377 EARLIER FILING DATE: 1998-03-10 NUMBER OF SEQ ID NOS: 11 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                              LENGTH: 566
TYPE: PRT
ORGANISM: Rabbit
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                                          Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                         Sequence 26, Application Patent No. 6800483
                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                             TYPE: PRT
ORGANISM: Oryctolagus cuniculus
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                                         IleGluAlaGlyCysLysThrThrThrSerAlaValMetValHisCysLeuArgGlnLys
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                                                                                                                                 SerSerLeu------PheArgLysAsnThrLysSerLeuAlaGluLysIleAla
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SerGluAspCysLeuTyrLeuAsnIleTyrThrProAlaAspLeuThrLysArgGlyArg
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US-08-845-295A-2
; Sequence 2, Application
; Patent No. 5817490
; Patent No. 5817490
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                                               ZIP: 37662-5075
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
        COMPUTER: IBM Compatible OPERATING SYSTEM: Windows 95 SOTTWARE Microsoft Word CURRENT APPLICATION DATA:
                                                                                                                    NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bastman Chemical Company
STREET: P.O. Box 511
                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                     STATE: TO COUNTRY:
                                                                                                           CITY:
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APPLICATION NUMBER: US/08/845,295A FILING DATE: 25-April-97
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Percent Similarity:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017
PILING DATE: 17-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 30,346
REFERENCE/DOCKET NUMBER: 7043
TELECOMMUNICATION INFORMATION:
TELEPHONE: 423-229-6189
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                                                                                                                        TCCATCTTTGATGGGTCCGCCTGGCTGCCTATGAGGAC-----GTGCTGGTTGTGGTC
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        AACTGGGCCTTCAAGGACCAGGTGGCTGCTCTGTCCTGGGTCCAGAAGAACATCGAGTTC
                                                                                                                                                                                                   -----SerGluAspCysLeuTyrLeuAsnIleTyrTnrProAlaAspLeuThrLys 134
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PheGlyGlyAspProGlySerValThrIlePheGlyGluSerPheThrAlaGlyGlyGlu 234
                                             TATAATCTGACTGAGCAGTACCTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGACTC
                                                                    HisGlyAspGluIlePheServalPheGlyPheProLeuLeuLysGlyAsp------
                                                                                                                                                                                       CACGCTGATGAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGGACATTGTTATG
                                                                                                                                                                                                                                                                ProValLysLysLysAspLeuPheLeuAspLeuMetGlyAspValValPheGlyValPro
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                     TyrAspGlnGluGluGlyTyrLeuGlnIleGlyValAsnThrGlnAlaAlaLysArgLeu
                                                                                                                                TTCGAAGGAGCCACGGAGGAGGAGAAGTTACTGAGCCCGGAAGATGATGAAATACTGGGCT 1497
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Best Local Similarity:
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APPLICANT: Hubbs, John C.
TITLE OF INVENTION: Enzymai
TITLE OF INVENTION: Aecorb.
TITLE OF INVENTION: 2-Keto
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09140933 Patent No. 6022719
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/140,
FILING DATE: 27-August-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 423-229-1239
INFORMATION FOR SEQ ID NO: 2:
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CLASSIFICATION DATA:

RICH APPLICATION NUMBER: US 60/017,879; 08/845,295

RILING DATE: 17-May-96; 25-April-97

ATTORNEY/AGENT INFORMATION:

NAME: Cheryl J. Tubach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 38,346
REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION:
TELEPHONE: 423-229-6189
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TYPE: Amino Acid
TOPOLOGY: Linear
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STATE: Tennesse
COUNTRY: USA
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2-Keto-L-Gulonic
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                                                        TATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAGCAC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Hubbs, John C.
                                                                    TELEFAX: 423-229-1239 INFORMATION FOR SEQ ID NO:
                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,879; 08/845,295
EILING DATE: 17-May-96; 25-April-97
ATTORNEY/AGENT INFORMATION:
NAME: Cheryl J. Tubach
REGISTRATION NUMBER: 38,346
REPERENCE/DOCKET NUMBER: 70432
                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Enzymatic Process for the Manufacture of TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and TITLE OF INVENTION: Acid NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
             SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                             ZIP: 37662-5075
COMPUTER READABLE FORM:
MEDIUM TYPB: 3.5 inch disk
                                                                                             TELEPHONE: 423-229-6189
 MOLECULE TYPE:
                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/14 FILING DATE: 03-Septmeber-98
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CITY: Kingsport
                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Eastman Chemical Company STREET: P.O. Box 511
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Best Local Similarity:
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                            GlnIleAlaValLeuAlaGlyCysLysThrThrThrSerAlaValPheThrPheValHis
                                                                                GluSerGlyValAlaLeuThrValAlaLeuValArgLysAspMetLysAlaAlaAlaLys
                                                                                                                                          AGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTATTCCACAAAGCCATCATG
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AsnTrpGlyHisLeuAspGlnValAlaAlaLeuHisTrpValGlnGluAsnIleAlaAsn
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US-09-150-515-2
                                                Sequence 2, Application US/09150515
Fatent No. 6271006
GENERAL INFORMATION:
APPLICANT: Hubbs, John C.
TITLE OF INVENTION: Enzymatic Process for the Manufacture of TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eastman Chemical Company
STREET: P.O. Box 511
CITY: Kingsport
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 584 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
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APPLICATION NUMBER: US 60/017,879;

FILING DATE: 17-MAY-96; 25-April-97

ATTORNEY/AGENT INFORMATION:

NAME: Cheryl J. Tubach

REGISTRATION NUMBER: 38,346

REFERENCE/DOCKET NUMBER: 70432
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
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                                                                        GGCTCCAAGCTCCCCGTCTTGGTGTGGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCC 480
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                                                                                                        TATTTGCACCTTGTGGCTAATGAATACTTCCATGACAAGCAC-----TCC
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                            GlnTyrArgProSerPheSerSerAspLysPheThrLysProLysThrValIleGlyAsp
                                                                                      CGGCACCGGCCTCAGTGCTTTGAAGAC-----ACGAAGCCGGCTTTTGTCAAAGCCGAC
                                                                                                                                                                                     GluLeuThrProValAlaThr-----PheThrAspLysTyrLeuGlyGlyThrAspAsp
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                                                                                                                                                                                                                                                                MetGlyPheProLeuSerGluGlyLysLeuAspGlnLysThrAlaThrSerLeuLeuTrp
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                                               CACGCTGATGAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATG
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US-09-264-737-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Engineering Plant Resistance to Pyridines
TITLE OF INVENTION: Expression of Esterase Enzymes
FILE REFERENCE: 38-21 (1053) RLE3 Pyridine Tolerance
CURRENT APPLICATION NUMBER: US/09/264,737A
CURRENT FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: 60/077,377
EARLIER FILING DATE: 1998-03-10
NUMBER OF SEQ ID NOS: 11
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application Patent No. 6107549 GENERAL INFORMATION:
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ORGANISM: Rabbit
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                                                                                                     TCAGAAGACTGCCTCTACCTGAACATCTATGCGCCTGCCCACGCCGATACAGGCTCCAAG
                                                                                                                                                                                                         AsnThrThrSerTyrProProMetCysSerSerAspAla------ValSerGly 76
                                                                                                                                                                                                                                                                          ProLeuGlySerLeuArgPheAlaProProGlnProAlaGluSerTrpSerHisValLys
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                     CTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACGGAGGAGGAGGAAGTTACTGAGCCGG 1476
                                                                CCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTCCGCTTTGTGTTCGGTGGTGCCTTC 1416
                                                                                                                                                                  GGTGCACCTGTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTGCTTTGAAGACACGAAG 1356
                                                                                                                                                                                                  CTTGGAGATGTGTTCTTTGTGGTCCCTGCACTGATCACAGCTCGATATCACAGAGATGCT 1296
                                                                                                                                                                                                                                                                      GluLysTyrLeuGlyGlyThrAspAspProValLysLysLysAspLeuPheLeuAspMet 393
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US-08-446-100-26
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Patent No.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME: Hendricks, Glenna
REGISTRATION UNMBER: 32,535
REFERENCE/DOCKET NUMBER: broo
TELECOMMUNICATION INFORMATION:
TELEPIONE: (703) 425-4250
TELEFAX: (703) 425-2767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of the protection of t
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ZIP: 22031
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                   No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 9669 / CITY: Fairfax
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US-08-446-100-28
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                                                                       Query Match:
                                                                                    Best Local Similarity:
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                                                                                                                                                                          US-08-446-100-28
                                                                                                                                Pred. No.:
                                                                                                   Percent Similarity:
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INFORMATION FOR SEQ ID NO: 28
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/446
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/JOCKET NUMBER: broo
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CORRESPONDENCE ADDRESS: ADDRESS: Hendricks and Assoc.
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                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Re-lease #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22031
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ORIGINAL SOURCE:
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HYPOTHETICAL: YES
ANTI-SENSE: YES
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COUNTRY:
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                                                                                                                                    CTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAGTTTCGG 1326
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                 Query Match:
DB:
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Best Local Similarity:
                                                                                                                                                        US-08-446-100-30
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GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
APPLICANT: Lockridge, Oksana
TTTLE OF INVENTION: Site-Directed Mutagenesis of Esterases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
CCLASSIFICATION: 435
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TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: (
                                                                                                                                                                                      MOLECULE TYPE: P
HYPOTHETICAL: YE
ANTI-SENSE: YES
FRAGMENT TYPE: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-4250
                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,9
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 9669 A
CITY: Fairfax
STATE: VA
COUNTRY: US
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NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                      Мо.
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                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
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Matches:
                                                   Conservative: Mismatches:
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|GluThrGlnArgHisSerThrLeuLeuGlyThrVallIeAspGlyMetLeuLeuLeuLys 217
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|GluGluGluLeuLeuGluThrThrLeuLysIleGlyAsnSerTyrLeuTrpThrTyrArg
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                                                          ProLeuAlaLysAsnLeuPheHisArgAlaIleSerGluSerGlyValAlaLeuThrSer 140
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|||||||||::: 432 AlaPheTrpThrAsn 436
                                    CAGTACCTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGGTG 1626
                                                                                                                             GCCACGGAGGAGAAGTTACTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCT 1506
                                                                                          GATTTTTGGACCAGC 1641
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Search completed: June 15, 2005, 08:57:41 Job time : 53.3868 secs



Result

Query

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-Q-/cgn2 1/USPTO_spool/6664091/runat 14062005 133501 9433/app_query.fasta 1.4238
-DB=PublIshed_Applications_AA._QFMT=fastan -SUFFIX=n2p.rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=bitsum62
-TRANS=human40.cdd -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEX=2000000000 -USER=6664091 @CGN 1 1 295 @runat 14062005 133501 9433
-NCPU=6 -ICPU=3 -NO_WAAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5. -DELOP=6 -DELEXT=7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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US-10-023-515-2
US-10-023-515-2
; Sequence 2, Application US/10023515
; Publication No. US20020182636A1
; GENERAL INFORMATION:
APPLICANT: Curtis, ROTY A. J.
APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
; TITLE OF INVENTION: 53010, TOWEL HUMAN CARBOXYLESTERASE
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
PILE REFERENCE: 10448-122001
; CURRENT APPLICATION NUMBER: US/10/023,515
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/256,369
pRIOR APPLICATION NUMBER: 60/279,508
; PRIOR APPLICATION NUMBER: 60/279,508
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 581
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Sequence 2, Application US/10674636

Publication No. US20040086922A1

REPLICANT: Curtis, Rory A. J.

APPLICANT: Silos-Santiago, Inmaculada

ITILE OF INVENTION: 53010, A NOVEL HUMAN CARBO:

ITITLE OF INVENTION: FAMILY MEMBER AND USES THIFILE REFERENCE: 10448-122001

CURRENT APPLICATION NUMBER: US/10/674,636

CURRENT FILING DATE: 2003-09-29
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PRIOR PILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/256,369
PRIOR FILING DATE: 2000-12-18
PRIOR PILING DATE: 2000-12-18
PRIOR PILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 6
SOPTWARE: PRESEQ for Windows Version 4./
SEQ ID NO 2
LENGTH: 581
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: KATICHELL, Venkateswarlu
APPLICANT: S110s-Santiago, Inmaculada
APPLICANT: S110s-Santiago, Inmaculada
APPLICANT: E11asof, Scott D.
TITLE OF INVENTION: UROLOGICAL DISORDERS US:
TITLE OF INVENTION: UROLOGICAL DISORDERS US:
TITLE OF INVENTION: 1405, 636, 4421, 5410, ...
TITLE OF INVENTION: 33751, 52872, 14053, 20;
TITLE OF INVENTION: 15347, 115, 579, 15985,
TITLE OF INVENTION: 32720, 4809, 14303, 1688;
TITLE OF INVENTION: 2543, 9626, 13231, 3240
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INVENTION: UROLOGICAL DISCRDERS USING 44390, 54181, 211, 5687, 884,
INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
INVENTION: 55053
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                                             CCTGCACTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTATGAG 1320
                                                                                        SerLeuThrGluIleArgAspSerLeuLeuAspLeuLeuGlyAspValPhePheValVal
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PRIOR APPLICATION NUMBER: 60/257,048
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PRIOR PILING DATE: 2000-12-19
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PRIOR FILING DATE: 2000-12-09
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PRIOR APPLICATION NUMBER: 60/264,922
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PRIOR APPLICATION NUMBER: 60/281,535
PRIOR APPLICATION NUMBER: 60/280,622
PRIOR PILING DATE: 2001-04-04
PRIOR PILING DATE: 2001-04-04
PRIOR PILING DATE: 2001-05-28
NUMBER OF SEG ID NOS: 110
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SEG ID NO 91
LENGTH: 575
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US-10-451-168-91
S-equence 91, Application US/10451168
; Publication No. US20040091969A1
         Alignment Scores:
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 Percent Similarity:
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APPLICANT: SMITHKLINE BEECHAM P.1.C.
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50039
CURRENT PILING DATE: 2003-11-12
                                                       TYPE: PRT
ORGANISM: Homo
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RESULT 5
US-10-433-256-10

Sequence 10, Application US/10433256

Publication No. US20040081980A1

GENERAL INFORMATION:
APPLICANT: SANJANMALA, Madhusudan M.; YAO, Monique G. APPLICANT: AU-YOUNG, Janice K.; BAUGHN, Mariah R. APPLICANT: HAFALIA; April J.A.; TANG, Y. Tom APPLICANT: LEE, Ernestine A.; DING, Li
APPLICANT: HAFALIA; April J.A.; TANG, Y. Tom APPLICANT: LU, Dyung Aina M.; LAL, Preeti G. APPLICANT: WARREN, Bridget A.; YANG, Junning APPLICANT: GANDHI, Ameena R.; LU, Yan APPLICANT: GANDHI, Ameena R.; LU, Yan APPLICANT: ISON, Craig H.
APPLICANT: GANDHI, Ameena R.; LU, Yan APPLICATION NUMBER: US/10/433,256
CURRENT FILING DATE: 2003-05-30
PRIOR APPLICATION NUMBER: US/10/433,256
PRIOR RILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: US 60/254,308
PRIOR FILING DATE: 2000-12-08
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PRIOR PILLING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 60/257,713
PRIOR APPLICATION NUMBER: US 60/262,706
PRIOR APPLICATION NUMBER: US 60/262,706
PRIOR PILLING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 60/266,020
PRIOR FILLING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PERL PROGRAM
SEQ ID NO 10
LENGTH: 642
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 6538080C
US-10-433-256-10
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                   GluSerAlaGlyAlaIleSerValSerSerLeuIleLeuSerProMetAlaLysGlyLeu
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RESULT 6
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PRIOR APPLICATION NUMBER: PCT/USO1/49232
PRIOR FILING DATE: 2000-12-17
PRIOR APPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/257,048
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/260,482
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/264,922
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR APPLICATION NUMBER: 60/289,622
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 110
SEQ ID NO 92
LENGTH: 581
TYPE: PRT
ORGANISM: Homo Sapiens
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CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
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APPLICANT: SMITHKLINE BEECHAM p.1.c.
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: NOVEL COMPOUNDS
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14 TrpAlaIleTrpValLeuAlaAlaPro------ThrLy8Gly
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GGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGGGTCCGCCCTGGCTGCCTAT
                             HisMetLeuLysValHisTyrProLysPheGlyValSerGluAspCysLeuTyrLeuAsn
                                                                                                               GluAlaThrSerTyrProAsnLeuCysLeuGlnAsnSerGluTrpLeuLeuLeuAspGln
                                                                                                                       GAAGCCACCTCCTACCCTAATTTGTGCCTCCAGAACTCAGAGTGGCTGCTCTTAGATCAA
                                                                                                                                                                 CCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTGCGA
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Matches:
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GAGGACGTGCTGGTTGTGGTCGTCCAGTACCGGCTAGGAATATTTGGTTTCTTCACCACA
GluGluLysLeuLeuSerArgLysMetMetLysTyrTrpAlaThrPheAlaArgThr
                                                              GAGGAGGAGAAGTTACTGAGCCGGAAGATGATGAAATACTGGGCTACCTTTGCTCGAACC
                                                                                 CGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCCACG
                                                                                                                            CCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTGTCAAAGCCGACCACGCTGATGAAGTC 1392
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APPLICANT: SUGIYAM
APPLICANT: WAKAMAT
APPLICANT: SATO, H
APPLICANT: ISHII,
APPLICANT: ISHII,
APPLICANT: ISONO,
APPLICANT: HIO, YU
APPLICANT: WAGAI,
APPLICANT: WAGAI,
APPLICANT: WAGAI,
APPLICANT: TAWECHI
APPLICANT: SEKI, N
APPLICANT: SEKI, N
APPLICANT: SEKI, N
APPLICANT: SEKI, N
APPLICANT: MAGAHAR
APPLICANT: MAGAHAR
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APPLICANT: 10. YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAL, KEITCHI
APPLICANT: NAGAL, KEITCHI
APPLICANT: NAGAL, KEITCHI
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGHAD, YASUHIKO
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2375
LENGTH: 525
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                             US-10-023-515-3 (1-1746) x US-10-094-749-2375 (1-525)
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OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
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YAMAMOTO, JUN-ICHI
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                                                                                                                                                       CTTGCCCTCCATCTGATACAAAACATCCTGCACATCCCGCCTCAGTATTTTGCACCTTGTG
                                                                                                                                                                                       CysGlyPheLeuLeuProMetLysGluAlaProGluIleLeuSerGlySerAsnLysSer
                                                                                                                                                                                                                                     LeuLeuSerGlnLysAlaPheLysAlaIleProSerIleIleGlyValAsnAsnHisGlu
                                                                                                                                                                                                                                                  CTATTGTCTCAGAAAGCATTTAAAGCAATTCCTTCCATCATCGGAGTCAATAACCACGAG
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                       GCTGGTGCACCTGTCTACTTCTATGAGTTTCGGCACCGGCCTCAGTGCTTTGAAGACACG
                                                        TTGCTTGGAGATGTGTTCTTTGTGGTCCCTGCACTGATCACAGCTCGATATCACAGAGAT
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Publication No. US20040030110A1
GENERAL INFORMATION:
APPLICANT: Guo, Xiaojia
APPLICANT: Kekuda, Ramesh
APPLICANT: Kekuda, Ramesh
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APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT: MacDougall, John R.
APPLICANT: Rothenberg, Mark B.
ITITLE OF INVENTION: NO. US20040030110A1el Proteins and Nucleic Acids Encoding
FILE REFERENCE: 21402-322C
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/281,086
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR APPLICATION NUMBER: 60/281,136
PRIOR FILING DATE: 2001-04-03
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Miller, Charles E.
Malyankar, Uriel M.
Spytek, Kimberly A.
Patturajan, Meera
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Shimkete, Richard A.
Gangolli, Esha A.
Taupier Jr., Raymond J
Casman, Stacie J.
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Gorman, Linda
Shenoy, Suresh G.
Pena, Carol E.A.
Smithson, Glennda
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Edinger, Shlomit R.
Stone, David J.
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Li, Li
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Gusev, Vladimir Y.
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PRIOR APPLICATION NUMBER: 60/281,906
PRIOR PILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/282,020
PRIOR APPLICATION NUMBER: 60/282,930
PRIOR PILING DATE: 2001-04-06
PRIOR PILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/282,934
PRIOR PILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/283,512
PRIOR APPLICATION NUMBER: 60/283,710
PRIOR APPLICATION NUMBER: 60/283,710
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR RILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,234
PRIOR PILING DATE: 2001-04-17
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Best Local Similarity:
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RESULT 9
US-10-381-898-2
; Sequence 2, Application US/10381898
; Publication No. US20040086887A1
; GENERAL INFORMATION:
; APPLICANT: AZIMZAI, Yalda; BAUGHN,
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                                                                                                                                             TyrLeuGlnLeuAspLeuAsnMetSerLeuGlyGlnArgLeuLysGluProArgArgAsp
                                                                                                                                                         TACCTCCAGCTGGACTTGAACATGAGCCTCGGACAGAGACTCAAAGAACCGCGGGGTGGAT 1629
                                                                                                                                                                                                                                                                                                     ValArgPheValPheGlyGlyAlaPheLeuLysGlyAspIleValMetPheGluGlyAla
                                                                                                                                                                                                                                                                                                                 GTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAAGGAGCC
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172 GlnHisMetLeuLysValHisTyrProLysPheGlyValSerGluAspCysLeuTyrLeu 172 GlnHisMetLeuLysValHisTyrProLysPheGlyValSerGluAspCysLeuTyrLeu 172 GlnHisMetLeuLysValHisTyrProLysPheGlyValSerGluAspCysLeuTyrLeu 172 GlnHisMetLeuLysValHisTyrProLysPheGlyValSerGluAspCysLeuTyrLeu	Qy 211 CCCCGCTGGGATCCCTGCGATTTACGAACCCGCAGCCTGCATCGCCCTGGGATAACTTG 270	Oy 151 GTCACTGTGCGGAAGCCCTGTGCAACGTGTTCCTCGGAGTCCCCTTTGCTGCT 210	91 GGGCCTTCTGCTGAAGGGCCACAGAGGAA 	81.66% 15 6) x US-10-381-89	Pred. No.: 5.59e-223 Length: 618 Pred. No.: 2588.50 Matches: 491 Percent Similarity: 94.62% Conservative: 1 Pest Total Girilarity: 04.46% Conservative: 5	; OFFIER INFORMATION: Incyte ID No: 7473645CD1 US-10-381-898-2		NUMBER OF SEQ ID NOS: 36 SOFTWARE: PERL Program SEQ ID NO 2 LENGTH: 618	; PRIOR APPLICATION NUMBER: US 60/252,834 ; PRIOR FILING DATE: 2000-11-22 ; PRIOR APPLICATION NUMBER: US 60/250,567 ; PRIOR FILING DATE: 2000-11-30	; PRIOR APPLICATION NUMBER: US 60/247,581 ; PRIOR FILING DATE: 2000-11-09 ; PRIOR APPLICATION NUMBER: US 60/249,519 ; PRIOR FILING DATE: 2000-11-16	; PRIOR APPLICATION NUMBER: US 60/238,864 ; PRIOR FILING DATE: 2000-10-06 ; PRIOR APPLICATION NUMBER: US 60/242,323 ; PRIOR FILING DATE: 2000-10-20	PRIOR APPLICATION NUMBER: PCT/US01/30662 PRIOR FILING DATE: 2001-09-28 PRIOR APPLICATION NUMBER: 06/236,947 PRIOR FILING DATE: 2000-09-29	TITLE OF INVENTION: DRUG METABÓLIZING ENZYMES FILE REFERENCE: PI-0233 USN CURRENT APPLICATION NUMBER: US/10/381,898 CTRRENT ETITIG DATE: 2003-10-17	APPLICANT: TANG, Y. Tom; TRIBOULEY, APPLICANT: CHAWLA, Narinder K.; WALS APPLICANT: WARREN, Bridget; XU, Yuni APPLICANT: YANG. Junming: YAO, Monig	APPLICANT: APPLICANT: APPLICANT: APPLICANT:	; APPLICANT: BOROWSKY, Mark L.; DING, Li; ; APPLICANT: DUGGAN, Brendan; BLLIOTT, Vicki S.; ; APPLICANT: GANDHI, Ameena R.; GRIFFIN, Jennifer A.; ; APPLICANT: HAFALIA, April J.A.; ISON, Craig H.; ; APPLICANT: KHAN, FATTAN A.; I.A.; Preet G.
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APPLICANT: CRESTARCH INSTITUTE

APPLICANT: REIIX RESEARCH INSTITUTE

ITILE OF INVENTION: NO. US20030236392Alel full length cDN

FILE REFERENCE: H1-A0105

CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT FILING DATE: 2002-03-25

PRIOR APPLICATION NUMBER:

PRIOR APPLICATION NUMBER:

PRIOR FILING DATE:

NUMBER OF SEQ ID NOS: 4096

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2219

LENGTH: 469

TYPE: PRT

ORGANISM: Homo sapiens

US-10-104-047-2219
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Best Local Similarity:
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Pred. No.:
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Sequence 2, Application US/10233933A
Publication No. US20040214171A1
GENERAL INFORMATION:
APPLICANT: Yamashita, Tetsuro
APPLICANT: Miyazaki, Masao
TITLE OF INVENTION: CAT KIDNEY DISEASE MARKER
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CURRENT APPLICATION NUMBER: US/10/233,933A
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: JP2002-057908
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
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                            GAGTCCGCGGGAGCCATAAGTGTTTCTAGTCTTATACTGTCTCCCATGGCCAAAGGCTTA
                                                                                                           TrpValArgAspAsnIleGluPhePheGlyGlyAspProArgSerValThrIlePheGly
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                                                 TTCCACAAAGCCATCATGGAGAGTGGGGTGGCCATCATCCCTTACCTG---GAGGCCCAT
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                           Sequence 4, Application US/10233933A
Publication No. US20040214171A1
GENERAL INFORMATION:
APPLICANT: Yamashita, Tetsuro
APPLICANT: Miyazaki, Masao
TITLE OF INVENTION: CAT KIDNEY DISEASE MARKER
FILE REFERENCE: SHIG FP02US006
CURRENT APPLICATION NUMBER: US/10/233,933A
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: DF2002-057908
PRIOR FILING DATE: 2002-04-03
NUMBER OF SEQ ID NOS: 4
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                                                                        GATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTTCTGTGGTAACAATGCGTCA
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                                                                                                                            GlyAspGluArgLysLysAspLeuGlnValLeuAlaArgIleCysGlyCysHisAlaSer
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 SerLysLysLeuThrPheSerIleProValIleAspAspPhePhePheProAspGluPro
                                          AGCCAGAAAACAAAGTCTTTCACTCGAGTGGTTGATGGTGCTTTTCTTTTCCTAATGAGCCT
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71.73%
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Conservative:
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                               PRIOR APPLICATION NUMBER: PCT/USO1/49232
PRIOR FILING DATE: 2000-12-17
PRIOR PEPLICATION NUMBER: 60/256,710
PRIOR FILING DATE: 2000-12-19
PRIOR REPLICATION NUMBER: 60/257,048
PRIOR FILING DATE: 2000-12-20
PRIOR PEPLICATION NUMBER: 60/260,482
PRIOR FILING DATE: 2001-01-09
PRIOR PPLICATION NUMBER: 60/264,922
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR APPLICATION NUMBER: 60/266,797
PRIOR FILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-03-19
PRIOR PILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR PILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR APPLICATION NUMBER: 60/276,988
PRIOR PILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/281,535
PRIOR APPLICATION NUMBER: 60/281,535
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US-10-451-168-93
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CURRENT APPLICATION NUMBER: US/10/451,168
CURRENT FILING DATE: 2003-11-12
                                                                                                                                                                                                                                                                                 APPLICANT: SMITHKLINE BEECHAM CORPORATION APPLICANT: SMITHKLINE BEECHAM p.l.c. APPLICANT: GLAXO GROUP LIMITED
                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL COMPOUNDS
FILING DATE: 2001-04-04
APPLICATION NUMBER: 60/289,622
FILING DATE: 2002-06-28
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; SOFWARE: FastSEQ for Windows Version
; SEQ ID NO 93
; LENGTH: 356
; TYPE: PAT
; ORGANISM: Homo sapiens
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Best Local Similarity:
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                                      GlyAlaThrGluGluLysLeuLeuSerArgLysMetMetLysTyrTrpAlaThrPhe
                                                                                      GATGAAGTCCGCTTTGTGTTCGGTGGTGCCTTCCTGAAGGGGGACATTGTTATGTTCGAA 1443
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                                                                           ArgHisArgProGlnCysPheGluAspThrLysProAlaPheValLysAlaAspHisAla
                                                                                                                                                      AlaLeuIleThrAlaArgTyrHisArgAspAlaGlyAlaProValTyrPheTyrGluPhe
                                                          GGAGCCACGGAGGAGGAGAAGTTACTGAGCCGGAAGATGATGAATACTGGGCTACCTTT
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Sequence 689, Application US/09925298

Publication No. US20020039764A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103
CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 689
LENGTH: 549
                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
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; OTHER INFORMATION:
US-09-925-298-689
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US-09-925-298-689
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LOCATION: (1)
OTHER INFORMATION: 1
NAME/KEY: SITE
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ORGANISM: Homo :
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ArgAspGlyThrThrHisProAlaMetCysLeuGlnAspLeuThrAlaValGluSerGlu
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; ORGANISM: Homo sapie;
; FRATURE:
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; NAME/KEY: SITE
; LOCATION: (1)
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US-10-102-806-689
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CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR PILING DATE: 2001-08-10
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PILING DATE: 1999-03-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
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                                                    ArgAspGlyThrThrHisProAlaMetCysLeuGlnAspLeuThrAlaValGluSerGlu 95
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1C 1377	1318 GAGTTTCGGCACCGGCCTCAGTGCTTTGAAGACACGAAGCCGGCTTTTTGTCAAAGCCGG ::: :::
NT 1317	1258 GTCCCTGCACTGATCACAGCTCGATATCACAGAGATGCTGGTGCACCTGTCTACTTCTI :::
NG 1257	1198 CACTCCCTGACTGAAATCCGAGACAGTCTTCTGGACTTGCTTG
kG 1197 3n 387	1138 ATCCTGCACATCCCGCCTCAGTATTTGCACCTTGTGGCTAATGAATACTTCCATGACAI::: ::: :::
1C 1137	1078 GAGGCTCCTGAGATCCTCAGTGGCTCCAACAAGTCCCTTGCCCTCCATCTGATACAAA; ::: 348 AspThrGlnLysGluMctAspArgGluAlaSerGlnAlaAlaLeuGlnLysMetLeuTh
NG 1077	1030 ATCATCGGAGTCAATAACCACGAGTGTGGCTTCCTGCTGCCTCATGAI
C 1029	970 TTCTTTCCTAATGAGCCTCTAGATCTATTGTCTCAGAAAGCATTTAAAGCAATTCCTTG
T 969	910 AAGGAGCTGCTGACCCTCAGCCAGAAAACAAAGTCTTTCACTCGAGTGGTTGATGGTGG
)C 909 /8 287	850 TGTGGTAACAATGCGTCAGACTCTGAGGCCCTGCTGAGGTGCCTGAGGACAAAACCCTC ::: 268 SerAlaCysAspGlnValAspSerGluAlaLeuValGlyCysLeuArgGlyLysSerLy
C 849	796 CTĠGAGGCCCATGATTATGAGAAGAGTGAGGACCTGCAGGTGGTTGCACATTT
C 795	736 ATGGCCAAAGGCTTATTCCACAAAGCCATCATGGAGAGTGGGGGTGGCCATCATCCCTTAC 795 :::::::
735 735 70 231	676 GTGACCATCTTTGGCGAGTCCGGGGGAGCCATAAGTGTTTTCTAGTCTTAATACTGTCTCG
УТ 675 .g 211	616 GTGGCTGCTCTGTGCTTGGGTCCAGAAGAACATCGAGTTCTTCGGTGGGGACCCCAGCTC
NG 615 191	556 TTTGGTTTCTTCACCACATGGGATCAGCATGCTCGGGGGAACTGGGCCTTCAAGGACCA
2A 555 11 171	496 TCCGCCCTGGCTGCCTATGAGGACGTGCTGGTTGTGGTCCTCCAGTACCGGCTAGGAAT
96 495 151	436 GTCTTGGTGTGTTCCCAGGAGGTGCCTTCAAGACTGGCTCAGCCTCCATCTTTGATGC
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